

GenCore version 5.1.9
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OM protein - protein search, using SW model

Run on: July 12, 2006, 05:39:35 ; Search time 49 Seconds
(without alignments)
26.795 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYLIG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

Database:

Issued Patents AA.*
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/8 COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/9 COMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/10 COMB.pep.*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfill1.pep.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	36	50.0	12	2	US-09-185-501B-6
2	27.5	38.2	14	2	US-09-305-781-2
3	27	37.5	9	3	US-09-641-528B-2131
4	27	37.5	9	3	US-09-641-528B-11725
5	27	37.5	9	3	US-09-641-528B-24500
6	27	37.5	10	3	US-09-641-528B-2132
7	27	37.5	10	3	US-09-641-528B-11726
8	27	37.5	10	3	US-09-641-528B-20365
9	27	37.5	10	3	US-09-641-528B-24501
10	27	37.5	11	3	US-09-641-528B-16759
11	27	37.5	11	3	US-09-641-528B-20366
12	27	37.5	11	3	US-09-641-528B-24535
13	27	37.5	11	3	US-09-641-528B-46330
14	27	37.5	15	3	US-09-641-528B-51190
15	27	37.5	12	1	US-08-463-966A-34
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Result No.	Score	Query Match	Length	DB ID	Description
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2	27.5	38.2	14	2	US-09-305-781-2
3	27	37.5	9	3	US-09-641-528B-2131
4	27	37.5	9	3	US-09-641-528B-11725
5	27	37.5	9	3	US-09-641-528B-24500
6	27	37.5	10	3	US-09-641-528B-2132
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-54

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 4 KSIYIG 9

RESULT 29
PCT-US93-11703-55
Sequence 55, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Miotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US93-11703-55

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 2 KSIYIG 7

RESULT 30
US-08-787-547-62
Sequence 62, Application US/08787547
Patent No. 5785567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-62

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
DB 5 VPSV 9

RESULT 31
US-08-417-174-48
Sequence 48, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

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APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-48

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
DB 5 VPFSV 9

RESULT 32
US-08-417-174-83
Sequence 83, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-83

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
DB 5 VPFSV 9

RESULT 33
US-08-417-174-84
Sequence 84, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2006, 05:39:35 : Search time 49 Seconds
(without alignments)
26.795 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

Database : Issued Patente_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27.5	38.2	14	US-09-305-781-2	Sequence 2, Appl1
3	27	37.5	9	US-09-641-528B-2131	Sequence 2131, Ap
4	27	37.5	9	US-09-641-528B-11725	Sequence 11725, A
5	27	37.5	9	US-09-641-528B-24500	Sequence 24500, A
6	27	37.5	10	US-09-641-528B-2132	Sequence 2132, Ap
7	27	37.5	10	US-09-641-528B-11726	Sequence 11726, A
8	27	37.5	10	US-09-641-528B-20365	Sequence 20365, A
9	27	37.5	10	US-09-641-528B-16759	Sequence 16759, A
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17	26	36.1	12	US-08-464-329A-34	Sequence 34, Appl
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265	22	30.6	15	1	US-08-129-607-1	Sequence 1, Appl1	338	21	29.2	10	2	US-09-935-430-262	Sequence 262, App
266	22	30.6	15	1	US-08-331-397B-36	Sequence 36, Appl	339	21	29.2	10	2	US-09-935-430-420	Sequence 420, App
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288	21	29.2	7	2	US-08-482-528-184	Sequence 184, App	361	21	29.2	11	2	US-09-239-043D-1030	Sequence 1030, Ap
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312	21	29.2	9	3	US-09-898-860-124	Sequence 124, App	385	21	29.2	12	2	US-09-394-019C-10	Sequence 10, Appl1
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572	20	27.8	12	2	US-09-394-019C-171	Sequence 171, App	645	20	26.4	8	3	US-09-641-5288-1494	Sequence 1494, App
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603	20	27.8	15	2	US-09-284-100A-20	Sequence 20, App	676	20	26.4	8	3	US-09-641-5288-40850	Sequence 40850, App
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606	20	27.8	15	2	US-09-500-135C-104	Sequence 104, App	679	20	26.4	8	3	US-09-641-5288-43763	Sequence 43763, App
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688	19	26.4	9	2	US-09-187-859-4005	Sequence 4005, Ap	761	19	26.4	9	3	US-09-641-528B-48874	Sequence 48874, A
689	19	26.4	9	2	US-09-604-957-11	Sequence 11, App1	762	19	26.4	9	3	US-09-641-528B-50005	Sequence 50005, A
690	19	26.4	9	2	US-09-390-134B-36	Sequence 36, App1	763	19	26.4	9	3	US-09-641-528B-50011	Sequence 50011, A
691	19	26.4	9	2	US-09-839-542B-3395	Sequence 3995, Ap	764	19	26.4	9	3	US-09-641-528B-50384	Sequence 50384, A
692	19	26.4	9	2	US-09-839-542B-4005	Sequence 4005, Ap	765	19	26.4	9	3	US-09-641-528B-51164	Sequence 51164, A
693	19	26.4	9	2	US-09-631-863A-96	Sequence 96, App	766	19	26.4	10	1	US-08-172-707-5	Sequence 5, App11
694	19	26.4	9	2	US-09-935-430-12	Sequence 12, App1	767	19	26.4	10	1	US-07-946-481-1	Sequence 1, App111
695	19	26.4	9	2	US-09-935-430-452	Sequence 452, App	768	19	26.4	10	1	US-08-412-865-5	Sequence 5, App111
696	19	26.4	9	2	US-09-935-430-456	Sequence 456, App	769	19	26.4	10	1	US-08-432-694-5	Sequence 5, App111
697	19	26.4	9	2	US-09-935-430-551	Sequence 551, App	770	19	26.4	10	1	US-08-476-505-5	Sequence 5, App111
698	19	26.4	9	2	US-09-995-749A-17	Sequence 17, App1	771	19	26.4	10	1	US-08-299-285-1	Sequence 1, App111
699	19	26.4	9	2	US-09-865-548A-55	Sequence 55, App1	772	19	26.4	10	1	US-08-299-285-2	Sequence 2, App111
700	19	26.4	9	2	US-09-799-250B-116	Sequence 116, App	773	19	26.4	10	1	US-08-229-285-20	Sequence 20, App11
701	19	26.4	9	2	US-09-799-250B-227	Sequence 227, App	774	19	26.4	10	1	US-08-229-285-22	Sequence 22, App11
702	19	26.4	9	2	US-09-799-250B-225	Sequence 255, App	775	19	26.4	10	1	US-08-131-057A-6	Sequence 6, App11
703	19	26.4	9	2	US-09-799-250B-255	Sequence 340, App	776	19	26.4	10	1	US-08-487-336-5	Sequence 5, App11
704	19	26.4	9	2	US-09-799-250B-330	Sequence 353, App	777	19	26.4	10	1	US-08-463-224-52	Sequence 52, App1
705	19	26.4	9	2	US-09-799-250B-421	Sequence 421, App	778	19	26.4	10	1	US-08-463-377-52	Sequence 52, App1
706	19	26.4	9	2	US-09-799-250B-521	Sequence 521, App	779	19	26.4	10	1	US-08-967-999-12	Sequence 12, App1
707	19	26.4	9	2	US-09-799-250B-624	Sequence 624, App	780	19	26.4	10	1	US-08-967-999-14	Sequence 14, App1
708	19	26.4	9	2	US-10-006-869-395	Sequence 3995, App	781	19	26.4	10	1	US-08-968-676-112	Sequence 112, App1
709	19	26.4	9	2	US-10-006-869-4005	Sequence 4005, Ap	782	19	26.4	10	1	US-08-941-553-5	Sequence 5, App11
710	19	26.4	9	2	US-09-641-528B-410	Sequence 410, App	783	19	26.4	10	1	US-08-985-126-1	Sequence 1, App11
711	19	26.4	9	3	US-09-641-528B-413	Sequence 413, App	784	19	26.4	10	1	US-08-985-126-2	Sequence 2, App11
712	19	26.4	9	3	US-09-641-528B-1								

Query Match 50.0%; Score 36; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPSVSAKSVK 10
DB 3 VPSVAGVVK 12

RESULT 2

US-09-305-781-2
Sequence 2, Application US/09305781
Patent No. 6358511
GENERAL INFORMATION:
APPLICANT: Klocman et al.
TITLE OF INVENTION: NOVEL INHIBITORS OF HIV INFECTION
FILE REFERENCE: 070165.0454
CURRENT APPLICATION NUMBER: US/09/305,781
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: 60/084,076
EARLIER FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 14
TYPE: PRT
ORGANISM: Human
US-09-305-781-2

Query Match 38.2%; Score 27.5; DB 2; Length 14;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 VPSVSAKSVKSL 13
DB 3 VPSVA-SVRSLY 14

RESULT 3

US-09-641-528B-2131
Sequence 2131, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bastejan
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2131
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-2131

Query Match 37.5%; Score 27; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
DB 1 SIADSIKTL 9

RESULT 4
US-09-641-528B-11725
Sequence 11725, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bastejan
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11725
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-11725

Query Match 37.5%; Score 27; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
DB 1 SIADSIKTL 9

RESULT 5
US-09-641-528B-24500
Sequence 24500, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bastejan
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24500
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-24500

Query Match 37.5%; Score 27; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
DB 1 SIADSIKTL 9

Db 1 STADSIKTL 9

```
RESULT 6
US-09-641-528B-2132
; Sequence 2132, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2132
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-2132
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSYSKL 12
Db 1 STADSIKTL 9

```
RESULT 7
US-09-641-528B-11726
; Sequence 11726, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11726
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-11726
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSYSKL 12

Db 1 STADSIKTL 9

```
RESULT 8
US-09-641-528B-20365
; Sequence 20365, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20365
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-20365
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSYSKL 12
Db 2 STADSIKTL 10

```
RESULT 9
US-09-641-528B-24501
; Sequence 24501, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24501
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-24501
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSVKSL 12
|:|:|:|
Db 1 S1ADS1K1TL 9

RESULT 10

US-09-641-528B-16759
; Sequence 16759, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16759
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-16759

Query Match 37.5%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 3 S1ADS1K1TL 11

RESULT 11

US-09-641-528B-20366
; Sequence 20366, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20366
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-20366

Query Match 37.5%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 2 S1ADS1K1TL 10

RESULT 12

US-09-641-528B-24535
; Sequence 24535, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24535
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-24535

Query Match 37.5%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 3 S1ADS1K1TL 11

RESULT 13

US-09-641-528B-46330
; Sequence 46330, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46330
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46330

Query Match 37.5%; Score 27; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 7 SIADSIKTL 15

RESULT 14
US-09-641-528B-51190
; Sequence 51190, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51190
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-51190

Query Match 37.5%; Score 27; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 3 SIADSIKTL 11

RESULT 15
US-08-257-528B-34
; Sequence 34, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: Sia, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michael H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-528B-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
|:|:|:|
Db 2 KSIYIG 7

RESULT 16
US-08-460-602A-34
; Sequence 34, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
; APPLICANT: Sia, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michael H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,602A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-460-602A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7

RESULT 17
US-08-463-966A-34
; Sequence 34, Application US/08463966A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,966A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-966A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7

RESULT 18
US-08-465-217A-34
; Sequence 34, Application US/08465217A
; Patent No. 5800822
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides

; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,217A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-465-217A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7

RESULT 19
US-08-464-329A-34
; Sequence 34, Application US/08464329A
; Patent No. 5817754
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,329A

FILED DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 2 KSLYIG 7

RESULT 20
US-08-462-507A-34
Sequence 34, Application US/08462507A
Patent No. 5876731
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 2 KSLYIG 7

RESULT 21
US-08-467-881A-34
Sequence 34, Application US/08467881A
Patent No. 5951966
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15

Db 2 KSIYIG 7

RESULT 22

US-09-563-222C-35
Sequence 35, Application US/09563222C
Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICHAEL B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 12
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222C-35

Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
Db 1 SASSVSSLYL 11

RESULT 23

US-08-218-025A-183
Sequence 183, Application US/08218025A
Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: P.O. Box 457, 321 No. 55567441sttown Road
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206

TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-183

Query Match 36.1%; Score 26; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
Db 1 KSIYIG 6

RESULT 24

US-10-198-053-500
Sequence 500, Application US/10198053
Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 500
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-500

Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 53.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PPSVAKSVKSLYL 14
Db 2 PYSLDK--SLYL 12

RESULT 25

PCT-US93-11703-51
Sequence 51, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-51

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLVIG 15
DB 10 KSIYIG 15

RESULT 26
PCT-US93-11703-52
Sequence 52, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-52

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLVIG 15
DB 8 KSIYIG 13

RESULT 27
PCT-US93-11703-53
Sequence 53, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-53

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLVIG 15
DB 6 KSIYIG 11

RESULT 28
PCT-US93-11703-54
Sequence 54, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-54

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 4 KSIYIG 9

RESULT 29
PCT-US93-11703-55
Sequence 55, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US93-11703-55

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7

RESULT 30
US-08-787-547-62
Sequence 62, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-62

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
|||||
Db 5 VPPSV 9

RESULT 31
US-08-417-174-48
Sequence 48, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

```

/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ TELEX: 421792
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/ US-08-417-174-48

Query Match          34.7%  Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFVS 5
        |||||
        5 VPFVS 9

Db

RESULT 32
US-08-417-174-83
/ Sequence 83, Application US/08417174
/ Patent No. 5844075
/ GENERAL INFORMATION:
/ APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
```

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ TELEX: 421792
/ INFORMATION FOR SEQ ID NO: 83:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/ US-08-417-174-83

Query Match          34.7%  Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFVS 5
        |||||
        5 VPFVS 9

Db

RESULT 33
US-08-417-174-84
/ Sequence 84, Application US/08417174
/ Patent No. 5844075
/ GENERAL INFORMATION:
/ APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ TELEX: 421792
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
```

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-84

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 34
US-08-417-174-85
Sequence 85, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-85

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 35

US-08-417-174-86
Sequence 86, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SBO ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-86

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 36
US-08-417-174-87
Sequence 87, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-87

Query Match
Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
Matches 5; Conservativity 100.0%; Pred. No. 5e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 37
US-08-417-174-88
Sequence 88, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-88

Query Match
Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
Matches 5; Conservativity 100.0%; Pred. No. 5e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 38
US-08-417-174-89
Sequence 89, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-89

Query Match
Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
Matches 5; Conservativity 100.0%; Pred. No. 5e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5

Db 5 VPFSV 9

```
RESULT 39
US-08-417-174-90
; Sequence 90, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-417-174-90

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 40
US-08-417-174-91
; Sequence 91, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
```

```
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-91
```

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

```
RESULT 41
US-08-417-174-92
; Sequence 92, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
```

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-92

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 42
US-08-417-174-93
Sequence 93, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-93

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 43
US-08-417-174-94
Sequence 94, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-94

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 44
US-08-417-174-95
Sequence 95, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND

;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS: 126
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 95:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;;
;; US-08-417-174-95

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 45
US-08-417-174-96
;; Sequence 96, Application US/08417174
;; Patent No. 5844075
;;
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 97:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid

;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 96:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;;
;; US-08-417-174-96

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 46
US-08-417-174-97
;; Sequence 97, Application US/08417174
;; Patent No. 5844075
;;
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 97:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid

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; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-97

Query Match          34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VPFSV 5
        |||||
Db      5 VPFSV 9

RESULT 47
US-08-417-174-98
; Sequence 98, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-98

Query Match          34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VPFSV 5
        |||||
Db      5 VPFSV 9

RESULT 48
US-08-417-174-99
; Sequence 99, Application US/08417174
```

```
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-99

Query Match          34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VPFSV 5
        |||||
Db      5 VPFSV 9

RESULT 49
US-08-417-174-100
; Sequence 100, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
```


COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-100

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 50
US-08-417-174-101
Sequence 101, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849

TELEX: 421792
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-101

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 51
US-08-417-174-102
Sequence 102, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-102

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 52
US-08-417-174-103
; Sequence 103, Application US/084117174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-103
Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
Db 5 VPFSV 9
RESULT 53
US-08-902-516-30
; Sequence 30, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1M 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-30
Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
Db 5 VPFSV 9
RESULT 54
US-09-036-582-27
; Sequence 27, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human gp100Pmel117 peptide
US-09-036-582-27
Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
Db 5 VPFSV 9
RESULT 55
US-09-183-706-31
; Sequence 31, Application US/09183706
; Patent No. 6245525
; GENERAL INFORMATION:
; APPLICANT: Marcelange, Valrie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR

FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/183,706
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 09/122,989
EARLIER FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-183-706-31

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPSV 9

RESULT 56
US-09-267-439-48
Sequence 48, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-48

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPSV 9

RESULT 57
US-09-267-439-83
Sequence 83, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-83

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPSV 9

RESULT 58
US-09-267-439-84
Sequence 84, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439
;; FILING DATE:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 84:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;; US-09-267-439-84

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFVS 5
Db 5 VPFVS 9

RESULT 59
US-09-267-439-85
;; Sequence 85, Application US/09267439
;; Patent No. 6270778
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439
;; FILING DATE:
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 85:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;; US-09-267-439-85

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFVS 5
Db 5 VPFVS 9

RESULT 60
US-09-267-439-86
;; Sequence 86, Application US/09267439
;; Patent No. 6270778
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 86:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-86

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 61
US-09-267-439-87
Sequence 87, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-87

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 62
US-09-267-439-88

Sequence 88, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-88

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 63
US-09-267-439-89
Sequence 89, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

```

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-09-267-439-89

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Query Match	34.7%	Score 25	DB 2	Length 9
Best Local Similarity	100.0%	Pred. No.	5e+05	
Matches	5	Conservative	0	Mismatches 0; Indels 0; Gaps 0

Qy	1	VPFSV	5
Db	5	VPFSV	9

RESULT 64
 US-09-267-439-90
 ; Sequence 90, Application US/09267439
 ; Patent No. 6270778
 ; GENERAL INFORMATION:
 APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
 APPLICANT: STEVEN A.
 TITLE OF INVENTION: MELANOMA ANTIGENS AND
 TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
 METHODS
 NUMBER OF INVENTION: 126
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/267,439
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/417,174
 FILING DATE: 05-APR-1995
 APPLICATION NUMBER: US/08/231,565
 FILING DATE: 22-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: CAROL M. GRUPPI
 REGISTRATION NUMBER: 37,341

```

? REFERENCE/DOCKET NUMBER: 2026-4124US1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 758-4800
? TELEFAX: (212) 751-6849
? TELEX: 421792
? INFORMATION FOR SEQ ID NO: 90:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 9
? TYPE: amino acid
? STRANDEDNESS: unknown
? TOPOLOGY: unknown
? MOLECULE TYPE: Peptide
US-09-267-439-90

```

Query Match	34.7%;	Score 25;	DB 2;	Length 9;
Best Local Similarity	100.0%;	Pred. No. 5e+05;		
Matches	5;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	VPFSV	5
Db	5	VPFSV	9

RESULT 65
US-09-267-439-91
; Sequence 91, Application US/09267439

;
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

;	TITLE OF INVENTION:	MELANOMA ANTIGENS AND
;	TITLE OF INVENTION:	THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;	TITLE OF INVENTION:	THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L. L. P.
STREET: 345 PARK AVENUE

```

; STATE: NEW YORK
; COUNTRY: USA

```

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPE
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-91

Query Match	34.7%;	Score 25;	DB 2;	Length 9;
Best Local Similarity	100.0%;	Pred. No.	5e+05;	

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 66
US-09-267-439-92

Sequence 92, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-92

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 67
US-09-267-439-93
Sequence 93, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS: 126
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-93

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 68
US-09-267-439-94
Sequence 94, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439

FILED DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-94

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
Db 5 VPFVS 9

RESULT 69
US-09-267-439-95
Sequence 95, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-95

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
Db 5 VPFVS 9

RESULT 70
US-09-267-439-96
Sequence 96, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-96

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
Db 5 VPFVS 9

RESULT 71
US-09-267-439-97
Sequence 97, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-97
Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSV 5
Db 5 VPFSV 9
RESULT 72
US-09-267-439-98
Sequence 98, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK

COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-98

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 73
US-09-267-439-99
Sequence 99, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELETYPE: 421792
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-99

Query Match 34.7% Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VPFVS 5
Db 5 VPFVS 9

RESULT 74
US-09-267-439-100
Sequence 100, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELETYPE: 421792
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-100

Query Match 34.7% Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VPFVS 5
Db 5 VPFVS 9

RESULT 75
US-09-267-439-101
Sequence 101, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELETYPE: 421792
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-101

Query Match 34.7% Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VPFVS 5
Db 5 VPFVS 9

RESULT 76
US-09-267-439-102
Sequence 102, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-102

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 77
US-09-267-439-103
Sequence 103, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-103

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 78
US-09-166-448-72
Sequence 72, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chaux, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Strobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
TITLE OF INVENTION: MAGS-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 72
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-448-72

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 79
US-09-567-995-31
Sequence 31, Application US/09567995
Patent No. 6303756
GENERAL INFORMATION:
APPLICANT: Martelange, Valrie

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/ APPLICANT: De Smet, Charles
/ APPLICANT: Boon-Falleur, Thierry
/ TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
/ FILE REFERENCE: I0461/7054
/ CURRENT APPLICATION NUMBER: US/09/567,995
/ CURRENT FILING DATE: 2000-05-10
/ PRIOR APPLICATION NUMBER: 09/183,706
/ PRIOR FILING DATE: 1998-10-30
/ NUMBER OF SEQ ID NOS: 43
/ SEQ ID NO 31
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-567-995-31
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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      5 VPFSV 9
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RESULT 80
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/ Sequence 5, Application US/09249272
/ Patent No. 6306640
/ GENERAL INFORMATION:
/ APPLICANT: Nicolette, Charles
/ TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
/ FILE REFERENCE: GA0152US
/ CURRENT APPLICATION NUMBER: US/09/249,272
/ CURRENT FILING DATE: 1999-02-11
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Natural epitope, melanoma antigen gp100 aas 209-217
US-09-249-272-5
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Query Match          34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 VPFSV 5
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Db      5 VPFSV 9
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Search completed: July 12, 2006, 05:40:40
Job time : 57 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

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Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYLIG 15

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Searched: 204771 seqs, 57208143 residues

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Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	24	33.3	12	7	US-11-254-679-92	Sequence 92, Appl
5	23	31.9	11	6	US-10-538-066-370	Sequence 370, Appl
6	23	31.9	12	6	US-10-522-086-21	Sequence 21, Appl
7	23	31.9	12	7	US-11-298-560-36	Sequence 36, Appl
8	22	30.6	9	6	US-10-538-066-374	Sequence 374, Appl
9	22	30.6	12	7	US-11-122-986-469	Sequence 469, Appl
10	22	30.6	12	7	US-11-122-986-506	Sequence 506, Appl
11	22	30.6	13	7	US-11-330-822-86	Sequence 86, Appl
12	22	30.6	15	7	US-11-122-986-737	Sequence 737, Appl
13	22	30.6	15	7	US-11-295-192A-730	Sequence 730, Appl
14	22	30.6	15	7	US-11-295-192A-731	Sequence 731, Appl
15	22	30.6	15	7	US-11-295-192A-732	Sequence 732, Appl
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17	22	30.6	15	7	US-11-295-192A-734	Sequence 734, Appl
18	22	30.6	15	7	US-11-295-192A-735	Sequence 735, Appl
19	22	30.6	15	7	US-11-295-192A-736	Sequence 736, Appl
20	22	30.6	15	7	US-11-295-192A-737	Sequence 737, Appl
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22	21	29.2	7	7	US-11-061-841-303	Sequence 303, Appl
23	21	29.2	9	6	US-10-781-659-24	Sequence 24, Appl
24	21	29.2	10	6	US-10-538-066-239	Sequence 239, Appl
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35	21	29.2	15	7	US-11-295-192A-481	Sequence 481, Appl
36	21	29.2	15	7	US-11-295-192A-482	Sequence 482, Appl
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44	21	29.2	15	7	US-11-290-070A-1	Sequence 1, Appl
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47	20	27.8	13	6	US-11-303-372-83	Sequence 83, Appl
48	20	27.8	15	7	US-11-303-372-84	Sequence 84, Appl
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51	19	26.4	9	7	US-11-140-487A-175	Sequence 175, Appl
52	19	26.4	9	7	US-11-140-487A-319	Sequence 319, Appl
53	19	26.4	9	7	US-11-140-487A-428	Sequence 428, Appl
54	19	26.4	9	7	US-11-140-487A-560	Sequence 560, Appl
55	19	26.4	9	7	US-11-140-487A-584	Sequence 584, Appl
56	19	26.4	9	7	US-11-140-487A-638	Sequence 638, Appl
57	19	26.4	9	7	US-11-140-487A-670	Sequence 670, Appl
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59	19	26.4	10	7	US-11-140-487A-1702	Sequence 1702, Appl
60	19	26.4	10	7	US-11-140-487A-1820	Sequence 1820, Appl
61	19	26.4	10	7	US-11-134-871-325	Sequence 325, Appl
62	19	26.4	11	6	US-10-953-613C-409	Sequence 409, Appl
63	19	26.4	12	6	US-10-953-613C-119	Sequence 119, Appl
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65	19	26.4	12	6	US-10-953-613C-127	Sequence 127, Appl
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109	18	25.0	7	6	US-10-981-300-39	Sequence 39, Appl	182	18	25.0	15	6	US-10-449-902-3977	Sequence 3497, A
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112	18	25.0	9	6	US-10-487-890-9	Sequence 9, Appl1	185	18	25.0	15	7	US-11-247-376-6	Sequence 6, Appl1
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114	18	25.0	9	6	US-10-953-613C-395	Sequence 395, App	187	18	25.0	15	7	US-11-140-487A-1199	Sequence 2199, Ap
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119	18	25.0	9	7	US-11-140-487A-295	Sequence 295, App	192	18	25.0	15	7	US-11-295-192A-202	Sequence 202, App
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121	18	25.0	9	7	US-11-140-487A-429	Sequence 429, App	194	18	25.0	15	7	US-11-295-192A-204	Sequence 204, App
122	18	25.0	9	7	US-11-140-487A-561	Sequence 561, App	195	18	25.0	15	7	US-11-295-192A-792	Sequence 792, App
123	18	25.0	9	7	US-11-140-487A-867	Sequence 867, App	196	18	25.0	15	7	US-11-295-192A-793	Sequence 793, App
124	18	25.0	9	7	US-11-140-487A-944	Sequence 944, App	197	18	25.0	15	7	US-11-295-192A-794	Sequence 794, App
125	18	25.0	9	7	US-11-251-465-82	Sequence 82, Appl	198	18	25.0	15	7	US-11-295-192A-795	Sequence 795, App
126	18	25.0	10	7	US-11-140-487A-1633	Sequence 1633, Ap	199	18	25.0	15	7	US-11-295-192A-896	Sequence 896, App
127	18	25.0	10	7	US-11-140-487A-1643	Sequence 1643, Ap	200	18	25.0	15	7	US-11-295-192A-897	Sequence 897, App
128	18	25.0	10	7	US-11-140-487A-1653	Sequence 1653, Ap	201	18	25.0	15	7	US-11-295-192A-898	Sequence 898, App
129	18	25.0	10	7	US-11-140-487A-1736	Sequence 1736, Ap	202	18	25.0	15	7	US-11-295-192A-900	Sequence 900, App
130	18	25.0	10	7	US-11-140-487A-1866	Sequence 1866, Ap	203	18	25.0	15	7	US-11-295-192A-901	Sequence 901, App
131	18	25.0	10	7	US-11-140-487A-1893	Sequence 1893, Ap	204	18	25.0	15	7	US-11-295-192A-902	Sequence 902, App
132	18	25.0	10	7	US-11-263-230-401	Sequence 401, App	205	18	25.0	15	7	US-11-295-192A-903	Sequence 903, App
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134	18	25.0	10	7	US-11-263-230-421	Sequence 421, App	207	18	25.0	15	7	US-11-295-192A-905	Sequence 905, App
135	18	25.0	10	7	US-11-263-230-431	Sequence 431, App	208	18	25.0	15	7	US-11-295-192A-906	Sequence 906, App
136	18	25.0	10	7	US-11-263-230-441	Sequence 441, App	209	18	25.0	15	7	US-11-295-192A-907	Sequence 907, App
137	18	25.0	10	7	US-11-263-230-451	Sequence 451, App	210	18	25.0	15	7	US-11-134-871-1120	Sequence 1120, Ap
138	18	25.0	10	7	US-11-263-230-461	Sequence 461, App	211	18	25.0	15	7	US-11-134-871-2165	Sequence 2165, Ap
139	18	25.0	10	7	US-11-263-230-471	Sequence 471, App	212	18	25.0	15	7	US-11-346-079-86	Sequence 86, Appl
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147	18	25.0	12	6	US-10-502-771-44	Sequence 44, Appl	220	17	23.6	7	7	US-11-061-841-307	Sequence 307, App
148	18	25.0	12	6	US-10-953-613C-111	Sequence 111, App	221	17	23.6	7	7	US-11-061-841-308	Sequence 308, App
149	18	25.0	12	6	US-10-953-613C-112	Sequence 112, App	222	17	23.6	7	7	US-11-061-841-309	Sequence 309, App
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152	18	25.0	12	6	US-10-953-613C-118	Sequence 118, App	225	17	23.6	7	7	US-11-061-841-313	Sequence 313, App
153	18	25.0	12	6	US-10-953-613C-121	Sequence 121, App	226	17	23.6	7	7	US-11-061-841-314	Sequence 314, App
154	18	25.0	12	6	US-10-953-613C-124	Sequence 124, App	227	17	23.6	7	7	US-11-259-123-87	Sequence 87, Appl
155	18	25.0	12	6	US-10-953-613C-125	Sequence 125, App	228	17	23.6	7	7	US-11-259-266-15	Sequence 15, Appl
156	18	25.0	12	6	US-10-953-613C-126	Sequence 126, App	229	17	23.6	7	7	US-11-259-267-15	Sequence 15, Appl
157	18	25.0	12	6	US-10-953-613C-132	Sequence 132, App	230	17	23.6	8	7	US-11-247-376-17	Sequence 17, Appl
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166	18	25.0	12	6	US-10-953-613C-219	Sequence 219, App	239	17	23.6	9	7	US-11-247-376-16	Sequence 16, Appl
167	18	25.0	12	6	US-10-953-613C-290	Sequence 290, App	240	17	23.6	9	7	US-11-140-487A-214	Sequence 214, Appl
168	18	25.0	12	6	US-10-953-613C-392	Sequence 392, App	241	17	23.6	9	7	US-11-140-487A-1126	Sequence 1126, Ap
169	18	25.0	12	6	US-10-953-613C-412	Sequence 412, App	242	17	23.6	9	7	US-11-140-487A-1429	Sequence 1429, Ap
170	18	25.0	12	7	US-11-122-986-799	Sequence 799, App	243	17	23.6	9	7	US-11-140-487A-1439	Sequence 1439, Ap
171	18	25.0	12	7	US-11-051-725-191	Sequence 191, App	244	17	23.6	9	7	US-11-140-487A-1632	Sequence 1632, Ap

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249	17	23.6	9	7	US-11-332-378-205	Sequence 205, App	322	17	23.6	15	7	US-11-247-376-4	Sequence 4, Appl1
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261	17	23.6	10	6	US-10-538-066-240	Sequence 240, App	334	17	23.6	15	7	US-11-247-376-25	Sequence 25, Appl1
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276	17	23.6	10	7	US-11-061-841-116	Sequence 116, App	349	17	23.6	15	7	US-11-295-192A-227	Sequence 227, App
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279	17	23.6	10	7	US-11-061-841-123	Sequence 123, App	352	17	23.6	15	7	US-11-295-192A-230	Sequence 230, App
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281	17	23.6	10	7	US-11-061-841-125	Sequence 125, App	354	17	23.6	15	7	US-11-295-192A-307	Sequence 307, App
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287	17	23.6	11	7	US-11-219-121-7	Sequence 7, Appl1	360	17	23.6	15	7	US-11-295-192A-313	Sequence 313, App
288	17	23.6	11	7	US-11-303-372-89	Sequence 89, Appl	361	17	23.6	15	7	US-11-295-192A-314	Sequence 314, App
289	17	23.6	11	7	US-11-303-372-96	Sequence 96, Appl	362	17	23.6	15	7	US-11-295-192A-315	Sequence 315, App
290	17	23.6	11	7	US-11-303-372-100	Sequence 100, Appl	363	17	23.6	15	7	US-11-295-192A-316	Sequence 316, App
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295	17	23.6	12	6	US-10-953-613C-230	Sequence 230, App	368	17	23.6	15	7	US-11-295-192A-895	Sequence 895, App
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297	17	23.6	12	7	US-11-176-182-115	Sequence 115, App	370	17	23.6	15	7	US-11-295-192A-1239	Sequence 1239, App
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336	16	22.2	9	6	US-10-536-804-49	Sequence 49, App1	469	16	22.2	12	7	US-11-281-666-70	Sequence 70, App1
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408	16	22.2	9	7	US-11-140-487A-680	Sequence 680, App	481	16	22.2	13	7	US-11-368-086-117	Sequence 117, App
409	16	22.2	9	7	US-11-140-487A-684	Sequence 684, App	482	16	22.2	14	6	US-10-499-266-17	Sequence 17, App1
410	16	22.2	9	7	US-11-140-487A-747	Sequence 747, App	483	16	22.2	14	7	US-11-122-986-361	Sequence 361, App
411	16	22.2	9	7	US-11-140-487A-875	Sequence 875, App	484	16	22.2	14	7	US-11-257-818-55	Sequence 55, App1
412	16	22.2	9	7	US-11-140-487A-888	Sequence 888, App	485	16	22.2	14	7	US-11-134-871-989	Sequence 989, App
413	16	22.2	9	7	US-11-140-487A-1116	Sequence 1116, App	486	16	22.2	14	7	US-11-134-871-3158	Sequence 3158, Ap
414	16	22.2	9	7	US-11-140-487A-1118	Sequence 1118, App	487	16	22.2	15	6	US-10-901-423-10	Sequence 10, App1
415	16	22.2	9	7	US-11-140-487A-1124	Sequence 1124, App	488	16	22.2	15	7	US-11-140-487A-2102	Sequence 2102, Ap
416	16	22.2	9	7	US-11-140-487A-1144	Sequence 1144, App	489	16	22.2	15	7	US-11-140-487A-2129	Sequence 2129, Ap
417	16	22.2	9	7	US-11-140-487A-1185	Sequence 1185, App	490	16	22.2	15	7	US-11-140-487A-2140	Sequence 2140, Ap
418	16	22.2	9	7	US-11-140-487A-1351	Sequence 1351, App	491	16	22.2	15	7	US-11-140-487A-2148	Sequence 2148, Ap
419	16	22.2	9	7	US-11-140-487A-1476	Sequence 1476, App	492	16	22.2	15	7	US-11-140-487A-2195	Sequence 2195, Ap
420	16	22.2	9	7	US-11-140-487A-1581	Sequence 1581, App	493	16	22.2	15	7	US-11-251-195-3	Sequence 3, App1
421	16	22.2	9	7	US-11-140-487A-1791	Sequence 1791, App	494	16	22.2	15	7	US-11-295-192A-79	Sequence 79, App1
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426	16	22.2	9	7	US-11-099-283B-408	Sequence 408, App	499	16	22.2	15	7	US-11-295-192A-84	Sequence 84, App1
427	16	22.2	10	7	US-11-301-554-2106	Sequence 2106, App	500	16	22.2	15	7	US-11-295-192A-85	Sequence 85, App1
428	16	22.2	10	7	US-11-140-487A-1079	Sequence 1079, App	501	16	22.2	15	7	US-11-295-192A-86	Sequence 86, App1
429	16	22.2	10	7	US-11-140-487A-1112	Sequence 1112, App	502	16	22.2	15	7	US-11-295-192A-87	Sequence 87, App1
430	16	22.2	10	7	US-11-140-487A-1117	Sequence 1117, App	503	16	22.2	15	7	US-11-295-192A-88	Sequence 88, App1
431	16	22.2	10	7	US-11-140-487A-1119	Sequence 1119, App	504	16	22.2	15	7	US-11-295-192A-89	Sequence 89, App1
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434	16	22.2	10	7	US-11-140-487A-1285	Sequence 1285, App	507	16	22.2	15	7	US-11-295-192A-109	Sequence 109, App
435	16	22.2	10	7	US-11-140-487A-1317	Sequence 1317, App	508	16	22.2	15	7	US-11-295-192A-110	Sequence 110, App
436	16	22.2	10	7	US-11-140-487A-1459	Sequence 1459, App	509	16	22.2	15	7	US-11-295-192A-111	Sequence 111, App
437	16	22.2	10	7	US-11-140-487A-1513	Sequence 1513, App	510	16	22.2	15	7	US-11-295-192A-112	Sequence 112, App
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440	16	22.2	10	7	US-11-140-487A-1535	Sequence 1535, App	513	16	22.2	15	7	US-11-295-192A-115	Sequence 115, App
441	16	22.2	10	7	US-11-140-487A-1594	Sequence 1594, App	514	16	22.2	15	7	US-11-295-192A-116	Sequence 116, App
442	16	22.2	10	7	US-11-140-487A-1671	Sequence 1671, App	515	16	22.2	15	7	US-11-295-192A-117	Sequence 117, App
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444	16	22.2	10	7	US-11-140-487A-1873	Sequence 1873, App	517	16	22.2	15	7	US-11-295-192A-119	Sequence 119, App
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447	16	22.2	10	7	US-11-122-986-39	Sequence 39, App1	520	16	22.2	15	7	US-11-295-192A-259	Sequence 259, App
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449	16	22.2	11	6	US-11-187-891-23	Sequence 23, App1	522	16	22.2	15	7	US-11-295-192A-261	Sequence 261, App
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453	16	22.2	11	6	US-11-122-986-532	Sequence 532, App	526	16	22.2	15	7	US-11-295-192A-265	Sequence 265, App
454	16	22.2	11	7	US-11-061-841-173	Sequence 173, App	527	16	22.2	15	7	US-11-295-192A-266	Sequence 266, App
455	16	22.2	11	7	US-11-061-841-183	Sequence 183, App	528	16	22.2	15	7	US-11-295-192A-728	Sequence 728, App
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539	15.5	21.5	11	7	US-11-061-841-48	Sequence 48, App1	612	15	20.8	9	7	US-11-155-929-124	Sequence 124, App
540	15.5	21.5	11	7	US-11-061-841-51	Sequence 51, App1	613	15	20.8	9	7	US-11-167-773-80	Sequence 80, App1
541	15.5	21.5	11	7	US-11-061-841-52	Sequence 52, App1	614	15	20.8	9	7	US-11-332-378-41	Sequence 41, App1
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543	15.5	21.5	11	7	US-11-061-841-61	Sequence 61, App1	616	15	20.8	9	7	US-11-332-170-1	Sequence 1, App1
544	15.5	21.5	11	7	US-11-061-841-62	Sequence 62, App1	617	15	20.8	9	7	US-11-340-431-67	Sequence 67, App1
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552	15	20.8	5	7	US-11-317-846-1	Sequence 1, App11	625	15	20.8	10	6	US-10-538-066-144	Sequence 143, App
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555	15	20.8	6	7	US-11-257-062-49	Sequence 49, App1	628	15	20.8	10	6	US-10-506-334-18	Sequence 18, App1
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562	15	20.8	7	7	US-11-061-841-299	Sequence 299, App	635	15	20.8	10	7	US-11-140-487A-1001	Sequence 1001, App
563	15	20.8	7	7	US-11-293-891-4	Sequence 4, App11	636	15	20.8	10	7	US-11-140-487A-1158	Sequence 1158, App
564	15	20.8	7	7	US-11-194-879-17	Sequence 17, App1	637	15	20.8	10	7	US-11-140-487A-1546	Sequence 1546, App
565	15	20.8	7	7	US-11-194-879-38	Sequence 38, App1	638	15	20.8	10	7	US-11-140-487A-1597	Sequence 1597, App
566	15	20.8	7	7	US-11-194-879-44	Sequence 44, App1	639	15	20.8	10	7	US-11-140-487A-1745	Sequence 1745, App
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568	15	20.8	8	6	US-10-714-343C-31	Sequence 31, App1	641	15	20.8	10	7	US-11-213-668-5	Sequence 5, App11
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574	15	20.8	8	7	US-11-294-583-2	Sequence 2, App11	647	15	20.8	10	7	US-11-263-230-445	Sequence 445, App
575	15	20.8	8	7	US-11-257-818-57	Sequence 57, App1	648	15	20.8	10	7	US-11-263-230-455	Sequence 455, App
576	15	20.8	8	7	US-11-336-555-6	Sequence 6, App11	649	15	20.8	10	7	US-11-263-230-465	Sequence 465, App
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578	15	20.8	9	1	US-09-906-4818-2	Sequence 2, App11	651	15	20.8	10	7	US-11-263-230-485	Sequence 485, App
579	15	20.8	9	6	US-10-497-088-12	Sequence 12, App1	652	15	20.8	10	7	US-11-263-230-503	Sequence 503, App
580	15	20.8	9	6	US-10-508-143A-2	Sequence 2, App11	653	15	20.8	10	7	US-11-263-230-521	Sequence 521, App
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596	15	20.8	9	7	US-11-140-487A-368	Sequence 368, App	669	15	20.8	11	7	US-11-263-537-110	Sequence 110, App1
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603	15	20.8	9	7	US-11-140-487A-1157	Sequence 1157, App	676	15	20.8	12	6	US-10-531-701-13	Sequence 13, App1
604	15	20.8	9	7	US-11-140-487A-1316	Sequence 1316, App	677	15	20.8	12	6	US-10-531-701-23	Sequence 23, App1
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606	15	20.8	9	7	US-11-140-487A-1744	Sequence 1744, App	679	15	20.8	12	6	US-10-953-613C-110	Sequence 110, App
607	15	20.8	9	7	US-11-140-487A-1816	Sequence 1816, App	680	15	20.8	12	6	US-10-953-613C-114	Sequence 114, App
608	15	20.8	9	7	US-11-140-487A-2058	Sequence 2058, App	681	15	20.8	12	6	US-10-953-613C-122	Sequence 122, App
609	15	20.8	9	7	US-11-155-929-52	Sequence 52, App1	682	15	20.8	12	6	US-10-953-613C-129	Sequence 129, App

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689	15	20.8	12	7	US-11-313-104-9	Sequence 9, Appl1
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699	15	20.8	13	7	US-11-313-356-13	Sequence 13, Appl1
700	15	20.8	13	7	US-11-134-871-649	Sequence 649, App
701	15	20.8	13	7	US-11-134-871-893	Sequence 893, App
702	15	20.8	13	7	US-11-373-720-18	Sequence 18, Appl1
703	15	20.8	14	6	US-10-489-071-3	Sequence 3, Appl1
704	15	20.8	14	7	US-11-213-668-3	Sequence 119, App
705	15	20.8	14	7	US-11-122-986-119	Sequence 16, Appl1
706	15	20.8	14	7	US-11-134-871-16	Sequence 1751, Ap
707	15	20.8	14	7	US-11-134-871-1751	Sequence 147, App
708	15	20.8	14	7	US-11-368-086-147	Sequence 148, App
709	15	20.8	14	7	US-11-368-086-148	Sequence 8, Appl1
710	15	20.8	15	6	US-10-490-949-5	Sequence 5, Appl1
711	15	20.8	15	6	US-10-544-499-5	Sequence 967, App
712	15	20.8	15	6	US-10-953-613C-967	Sequence 2209, Ap
713	15	20.8	15	7	US-11-140-487A-2209	Sequence 629, App
714	15	20.8	15	7	US-11-122-986-629	Sequence 66, Appl1
715	15	20.8	15	7	US-11-295-192A-66	Sequence 67, Appl1
716	15	20.8	15	7	US-11-295-192A-67	Sequence 68, Appl1
717	15	20.8	15	7	US-11-295-192A-68	Sequence 69, Appl1
718	15	20.8	15	7	US-11-295-192A-69	Sequence 70, Appl1
719	15	20.8	15	7	US-11-295-192A-70	Sequence 71, Appl1
720	15	20.8	15	7	US-11-295-192A-71	Sequence 72, Appl1
721	15	20.8	15	7	US-11-295-192A-72	Sequence 73, Appl1
722	15	20.8	15	7	US-11-295-192A-73	Sequence 74, Appl1
723	15	20.8	15	7	US-11-295-192A-74	Sequence 75, Appl1
724	15	20.8	15	7	US-11-295-192A-75	Sequence 91, Appl1
725	15	20.8	15	7	US-11-295-192A-91	Sequence 238, App
726	15	20.8	15	7	US-11-295-192A-238	Sequence 242, App
727	15	20.8	15	7	US-11-295-192A-242	Sequence 243, App
728	15	20.8	15	7	US-11-295-192A-243	Sequence 244, App
729	15	20.8	15	7	US-11-295-192A-244	Sequence 245, App
730	15	20.8	15	7	US-11-295-192A-245	Sequence 318, App
731	15	20.8	15	7	US-11-295-192A-318	Sequence 319, App
732	15	20.8	15	7	US-11-295-192A-319	Sequence 320, App
733	15	20.8	15	7	US-11-295-192A-320	Sequence 321, App
734	15	20.8	15	7	US-11-295-192A-321	Sequence 739, App
735	15	20.8	15	7	US-11-295-192A-739	Sequence 740, App
736	15	20.8	15	7	US-11-295-192A-740	Sequence 907, App
737	15	20.8	15	7	US-11-295-192A-907	Sequence 1175, Ap
738	15	20.8	15	7	US-11-295-192A-1175	Sequence 1177, Ap
739	15	20.8	15	7	US-11-295-192A-1176	Sequence 1178, Ap
740	15	20.8	15	7	US-11-295-192A-1177	Sequence 1179, Ap
741	15	20.8	15	7	US-11-295-192A-1178	Sequence 1180, Ap
742	15	20.8	15	7	US-11-295-192A-1179	Sequence 1181, Ap
743	15	20.8	15	7	US-11-295-192A-1180	Sequence 1182, Ap
744	15	20.8	15	7	US-11-295-192A-1181	Sequence 1183, Ap
745	15	20.8	15	7	US-11-295-192A-1182	Sequence 1184, Ap
746	15	20.8	15	7	US-11-295-192A-1183	Sequence 1185, Ap
747	15	20.8	15	7	US-11-295-192A-1184	Sequence 405, App
748	15	20.8	15	7	US-11-295-192A-1185	Sequence 73, Appl1
749	15	20.8	15	7	US-11-061-841-405	Sequence 945, App
750	15	20.8	15	7	US-11-350-752-73	Sequence 1196, Ap
751	15	20.8	15	7	US-11-350-749-73	Sequence 2537, Ap
752	15	20.8	15	7	US-11-134-871-945	Sequence 3091, Ap
753	15	20.8	15	7	US-11-134-871-1196	
754	15	20.8	15	7	US-11-134-871-2537	
755	15	20.8	15	7	US-11-134-871-3091	

756	15	20.8	15	7	US-11-134-871-3485	Sequence 3485, Ap
757	15	20.8	15	7	US-11-244-109-8	Sequence 8, Appl1
758	15	20.8	15	7	US-11-346-079-72	Sequence 72, Appl1
759	15	20.8	15	7	US-11-346-079-85	Sequence 85, Appl1
760	15	20.8	15	7	US-11-346-079-89	Sequence 89, Appl1
761	15	20.8	15	7	US-11-346-079-92	Sequence 92, Appl1
762	15	20.8	15	7	US-11-361-631-25	Sequence 25, Appl1
763	14.5	20.1	11	7	US-11-290-249-4	Sequence 4, Appl1
764	14	19.4	5	6	US-11-338-681-38	Sequence 38, Appl1
765	14	19.4	5	6	US-10-520-386-3	Sequence 3, Appl1
766	14	19.4	5	6	US-10-518-941-15	Sequence 15, Appl1
767	14	19.4	5	7	US-11-139-770A-7	Sequence 7, Appl1
768	14	19.4	6	6	US-10-525-126-17	Sequence 17, Appl1
769	14	19.4	6	6	US-10-953-613C-642	Sequence 642, App
770	14	19.4	6	6	US-10-953-613C-750	Sequence 750, App
771	14	19.4	6	7	US-11-257-818-20	Sequence 20, Appl1
772	14	19.4	6	7	US-11-257-818-29	Sequence 29, Appl1
773	14	19.4	6	7	US-11-317-846-10	Sequence 10, Appl1
774	14	19.4	6	7	US-11-327-214-13	Sequence 13, Appl1
775	14	19.4	7	6	US-10-546-594-94	Sequence 94, Appl1
776	14	19.4	7	6	US-10-522-086-23	Sequence 23, Appl1
777	14	19.4	7	7	US-11-271-008-2	Sequence 2, Appl1
778	14	19.4	7	7	US-11-254-679-81	Sequence 81, Appl1
779	14	19.4	7	7	US-11-023-959A-26	Sequence 26, Appl1
780	14	19.4	7	7	US-11-023-959A-56	Sequence 56, Appl1
781	14	19.4	7	7	US-11-023-959A-59	Sequence 59, Appl1
782	14	19.4	7	7	US-11-094-132-50	Sequence 50, Appl1
783	14	19.4	7	7	US-11-263-230-158	Sequence 158, App
784	14	19.4	7	7	US-11-263-230-160	Sequence 160, App
785	14	19.4	7	7	US-11-263-230-143	Sequence 1140, Ap
786	14	19.4	7	7	US-11-263-230-1144	Sequence 1144, Ap
787	14	19.4	7	7	US-11-263-230-1145	Sequence 1145, Ap
788	14	19.4	7	7	US-11-263-230-1146	Sequence 1146, Ap
789	14	19.4	7	7	US-11-263-230-1147	Sequence 1147, Ap
790	14	19.4	7	7	US-11-263-230-1148	Sequence 1148, Ap
791	14	19.4	7	7	US-11-263-230-1261	Sequence 1261, Ap
792	14	19.4	7	7	US-11-261-173-7	Sequence 7, Appl1
793	14	19.4	7	7	US-11-194-879-5	Sequence 5, Appl1
794	14	19.4	7	7	US-11-194-879-29	Sequence 29, Appl1
795	14	19.4	7	7	US-11-194-879-50	Sequence 50, Appl1
796	14	19.4	8	6	US-10-560-723-185	Sequence 185, App
797	14	19.4	8	6	US-10-449-902-25188	Sequence 29188, A
798	14	19.4	8	7	US-11-122-986-787	Sequence 787, App
799	14	19.4	8	7	US-11-122-986-787	Sequence 44, Appl1
800	14	19.4	8	7	US-11-194-879-39	Sequence 39, Appl1

ALIGNMENTS

```
RESULT 1
US-10-536-804-74
; Publication 74, Application US/10536804
; Publication No. US20060127908A1
; GENERAL INFORMATION:
; APPLICANT: Williamson, Magali
; TITLE OF INVENTION: Cancer Associated Plexin Bi Mutations
; FILE REFERENCE: 620-373
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: PCT/GB2003/005223
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: GB 0227908.1
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74
; LENGTH: 15
; TYPE: PR
; ORGANISM: Drosophila melanogaster
US-10-536-804-74
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Query Match 40.3%; Score 29; DB 6; Length 15;
Best Local Similarity 53.8%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|||||
Db 3 PFSMKPSVNBIDL 15

RESULT 2

US-10-536-804-76
; Sequence 76, Application US/10536804
; Publication No. US20060127908A1
; GENERAL INFORMATION:
; APPLICANT: Williamson, Magali
; APPLICANT: Masters, John
; TITLE OF INVENTION: Cancer Associated Plexin B1 Mutations
; FILE REFERENCE: 620-373
; CURRENT APPLICATION NUMBER: US/10/536,804
; PRIOR FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: PCT/GB2003/005223
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: GB 0227908.1
; PRIOR FILING DATE: 2002-11-29
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-536-804-76

Query Match 36.1%; Score 26; DB 6; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|||||
Db 3 PFSORPSVHALDL 15

RESULT 3

US-11-257-951-1
; Sequence 1, Application US/11257951
; Publication No. US20060140983A1
; GENERAL INFORMATION:
; APPLICANT: Palucka, Anna Karolina
; APPLICANT: Bancheureau, Jacques
; TITLE OF INVENTION: DENDRITIC CELLS LOADED WITH HEAT SHOCKED MELANOMA CELL BODIES
; FILE REFERENCE: BHCS 1013
; CURRENT APPLICATION NUMBER: US/11/257,951
; CURRENT FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: US 60/621,957
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-257-951-1

Query Match 34.7%; Score 25; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 4
US-11-254-679-92
; Sequence 92, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Klener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGBl and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 92
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-254-679-92

Query Match 33.3%; Score 24; DB 7; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLYL 14
::|||:|||||
Db 3 SOSVSTYL 11

RESULT 5

US-10-538-066-370
; Sequence 370, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.01SPC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 370
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-370

Query Match 31.9%; Score 23; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|||:|||||
Db 5 PFSVAK 10

RESULT 6
US-10-522-086-21
; Sequence 21, Application US/10522086
; Publication No. US20060121022A1
; GENERAL INFORMATION:
; APPLICANT: Koga, Takaki
; APPLICANT: Suzuki, Tsukasa
; APPLICANT: Saito, Hiroyuki
; TITLE OF INVENTION: NON-NEUTRALIZING ANTI-aPC ANTIBODIES
; FILE REFERENCE: 14875-138US1
; CURRENT APPLICATION NUMBER: US/10/522,086
; PRIOR FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: PCT/JP2003/009087
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: JP 2002-212582
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-522-086-21

Query Match 31.9%; Score 23; DB 6; Length 12;
Best Local Similarity 45.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 SVAKSVKSLYL 14
: : ||| :
Db 1 TASSSVSSSYL 11

RESULT 7
US-11-298-560-36
; Sequence 36, Application US/11298560
; Publication No. US20060115474A1
; GENERAL INFORMATION:
; APPLICANT: Jacquemin, Marc
; APPLICANT: Saint-Remy, Jean-Marie
; TITLE OF INVENTION: Ligands For Use In Therapeutic Compositions For The Treatment of
; TITLE OF INVENTION: Hemostasis Disorders
; FILE REFERENCE: 50304/110001
; CURRENT APPLICATION NUMBER: US/11/298,560
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 10/030,522
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP2000/06677
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/143,891
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: GB9916450.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: PCT/BE2004/000118
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: GB0319118.6
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: GB0319345.5
; PRIOR FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: KR1X-1 light chain CDR1
US-11-298-560-36

Query Match 31.9%; Score 23; DB 7; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AKSVKSLYL 14
: : ||| :
Db 3 SSVASAVYL 11

RESULT 8
US-10-538-066-374
; Sequence 374, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Erimune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 374
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-374

Query Match 30.6%; Score 22; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFSVA 6
: : ||| :
Db 5 PENVA 9

RESULT 9
US-11-122-986-469
; Sequence 469, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 469
; LENGTH: 12
; TYPE: PRT

ORGANISM: Enterococcus faecalis
US-11-122-986-469

Query Match 30.6%; Score 22; DB 7; Length 12;
Best Local Similarity 66.7%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAK 7
| | | |
DB 7 PFGVCK 12

RESULT 10

US-11-122-986-506
Sequence 506, Application US/11122986
Publication No. US20060104989A1
GENERAL INFORMATION:

APPLICANT: EDWARDS, ALED
APPLICANT: DHARAMSI, AKIL
APPLICANT: VEDADI, MASOUD
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
FILE REFERENCE: IPT-330.01
CURRENT APPLICATION NUMBER: US/11/122,986

PRIOR FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 60/423,875
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,832
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,915
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,757
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,758
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/424,367
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,376
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,370
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,362
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,373
PRIOR FILING DATE: 2002-11-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 844
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 506
LENGTH: 12
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-11-122-986-506

Query Match 30.6%; Score 22; DB 7; Length 12;
Best Local Similarity 66.7%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAK 7
| | | |
DB 7 PFGVCK 12

RESULT 11

US-11-330-822-86
Sequence 86, Application US/11330822
Publication No. US20060150281A1
GENERAL INFORMATION:

APPLICANT: GUAN, HANPING
APPLICANT: KEELING, PETER L.
TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
FILE REFERENCE: 15053-04
CURRENT APPLICATION NUMBER: US/11/330,822

CURRENT FILING DATE: 2006-01-11
PRIOR APPLICATION NUMBER: PCT/US98/06660
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/042,939
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 86
LENGTH: 13
TYPE: PRT
ORGANISM: Zea mays
US-11-330-822-86

Query Match 30.6%; Score 22; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PSVAKSVKSL 12
| | | |
DB 4 FSLKXXXXKL 13

RESULT 12
US-11-122-986-737
Sequence 737, Application US/11122986
Publication No. US20060104989A1
GENERAL INFORMATION:

APPLICANT: EDWARDS, ALED
APPLICANT: DHARAMSI, AKIL
APPLICANT: VEDADI, MASOUD
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
FILE REFERENCE: IPT-330.01
CURRENT APPLICATION NUMBER: US/11/122,986
PRIOR FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 60/423,875
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,832
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,915
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,757
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,758
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/424,367
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,376
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,370
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,362
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,373
PRIOR FILING DATE: 2002-11-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 844
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 737
LENGTH: 15
TYPE: PRT
ORGANISM: Escherichia coli
US-11-122-986-737

Query Match 30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 54.5%; Pred. No. 9.3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
| | | |
DB 1 SALLVKNPYL 11

RESULT 13

```
US-11-295-192A-730
; Sequence 730, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 730
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-730
```

```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 VPFSAKS 8
    :|||:
Db 8 MPVSWAKT 15
```

```
RESULT 14
US-11-295-192A-731
; Sequence 731, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 731
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-731
```

```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 VPFSAKS 8
    :|||:
Db 7 MPVSWAKT 14
```

```
RESULT 15
US-11-295-192A-732
; Sequence 732, Application US/11295192A
; Publication No. US20060110803A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 732
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-732
```

```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 VPFSAKS 8
    :|||:
Db 6 MPVSWAKT 13
```

```
RESULT 16
US-11-295-192A-733
; Sequence 733, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 733
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-733
```

```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 VPFSAKS 8
    :|||:
Db 5 MPVSWAKT 12
```

```
RESULT 17
US-11-295-192A-734
; Sequence 734, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
```

```

; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 734
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-734
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      4 MPVSMAKT 11
```

```

RESULT 18
US-11-295-192A-735
; Sequence 735, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 735
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-735
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      3 MPVSMAKT 10
```

```

RESULT 19
US-11-295-192A-736
; Sequence 736, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
```

```

; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 736
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-736
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      2 MPVSMAKT 9
```

```

RESULT 20
US-11-295-192A-737
; Sequence 737, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 737
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-737
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      1 MPVSMAKT 8
```

```

RESULT 21
US-11-294-583-19
; Sequence 19, Application US/11294583
; Publication No. US20060122122A1
; GENERAL INFORMATION:
; APPLICANT: TOGOSSEI CO., LTD
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND USE THEREOF
; FILE REFERENCE: TESHPI02US
; CURRENT APPLICATION NUMBER: US/11/294,583
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: 2004-352385
; PRIOR FILING DATE: 2004-12-06
; NUMBER OF SEQ ID NOS: 37
```



```
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-239

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 FSVAKSVKSLYLIG 15
DB      3 FNTLKPIFKLPLIG 15

RESULT 27
US-11-295-192A-240
; Sequence 240, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-240

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 FSVAKSVKSLYLIG 15
DB      2 FNTLKPIFKLPLIG 14

RESULT 28
US-11-295-192A-241
; Sequence 241, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
```

```
; CURRENT APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-241

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 FSVAKSVKSLYLIG 15
DB      1 FNTLKPIFKLPLIG 13

RESULT 29
US-11-295-192A-475
; Sequence 475, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 475
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-475

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFS 4
DB      12 VPFS 15

RESULT 30
US-11-295-192A-476
; Sequence 476, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
```

; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 476
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-476

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
 |||||
Db 11 VPFS 14

RESULT 31
US-11-295-192A-477
; Sequence 477, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 477
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-477

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
 |||||
Db 10 VPFS 13

RESULT 32
US-11-295-192A-478
; Sequence 478, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 478
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-478

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
 |||||
Db 9 VPFS 12

RESULT 33
US-11-295-192A-479
; Sequence 479, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-479

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
 |||||
Db 8 VPFS 11

RESULT 34
US-11-295-192A-480
; Sequence 480, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 480
; LENGTH: 15
; TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-480

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 7 VPPS 10

RESULT 35
US-11-295-192A-481
Sequence 481, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 481
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-481

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 6 VPPS 9

RESULT 36
US-11-295-192A-482
Sequence 482, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 482
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide

US-11-295-192A-482

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 5 VPPS 8

RESULT 37
US-11-295-192A-483
Sequence 483, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 483
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-483

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 4 VPPS 7

RESULT 38
US-11-295-192A-484
Sequence 484, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 484
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-484

Query Match 29.2%; Score 21; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
| | | |
Db 3 VPFS 6

RESULT 39

US-11-295-192A-485
; Sequence 485, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 485
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-485

Query Match 29.2%; Score 21; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
| | | |
Db 2 VPFS 5

RESULT 40

US-11-295-192A-486
; Sequence 486, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 486
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-486

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
| | | |
Db 1 VPFS 4

RESULT 41
US-11-295-192A-729
; Sequence 729, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 729
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-729

Query Match 29.2%; Score 21; DB 7; Length 15;

Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAK 7
: | : | |
Db 9 MPVSMAX 15

RESULT 42
US-11-295-192A-738
; Sequence 738, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-738

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAKS 8
| | : | | :
Db 1 PVSMAKT 7

```
RESULT 43
US-11-261-429-2
; Sequence 2, Application US/11261429
; Publication No. US20060115899A1
; GENERAL INFORMATION:
; APPLICANT: Buckner, Jane H.
; APPLICANT: Walker, Mindi R.
; TITLE OF INVENTION: METHODS OF GENERATING ANTIGEN-SPECIFIC CD4+CD25+ REGULATORY T
; FILE REFERENCE: BRIVM-1-26413
; CURRENT APPLICATION NUMBER: US/11/261,429
; PRIOR FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US 60/623,380
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-261-429-2

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      9 VMSLYL 14
|::|||
Db      4 VEALYL 9

RESULT 44
US-11-290-070A-1
; Sequence 1, Application US/11290070A
; Publication No. US20060115478A1
; GENERAL INFORMATION:
; APPLICANT: GREGG, Randall
; APPLICANT: ZAGHOUBI, Habib
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING AND PREVENTING TYPE-1
; FILE REFERENCE: 05062086
; CURRENT APPLICATION NUMBER: US/11/290,070A
; PRIOR FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 10/681,788
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/371,663
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: PCT/US03/10700
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Insulin B chain
US-11-290-070A-1.

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      9 VMSLYL 14
|::|||
Db      4 VEALYL 9

RESULT 45
US-11-099-283B-401
; Sequence 401, Application US/11099283B
```

```
; Publication No. US20060134744A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS
; FILE REFERENCE: 6680_014
; CURRENT APPLICATION NUMBER: US/11/099,283B
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Unknown amino acid
US-11-099-283B-401

Query Match          27.8%; Score 20; DB 7; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 VAKSVSLY 13
|::|||
Db      2 VXPVRSY 10

RESULT 46
US-11-254-679-98
; Sequence 98, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kiener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyne, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMG1 and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 12
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-11-254-679-98

Query Match      27.8%; Score 20; DB 7; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      6 AKSVKSLYL 14
       |||:|:|
DB      3 SOSVRSNFL 11

RESULT 47
US-10-564-619-2
; Sequence 2, Application US/10564619
; Publication No. US20060121083A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; TITLE OF INVENTION: ANTI-MICROBIAL MEDICAL IMPLANTS AND USES THEREOF
; FILE REFERENCE: 31019
; CURRENT APPLICATION NUMBER: US/10/564,619
; CURRENT FILING DATE: 2006-01-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: misc_feature
; OTHER INFORMATION: Possible amidation and aminolauryl added at C'
US-10-564-619-2

Query Match      27.8%; Score 20; DB 6; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AKSVKSL 12
       |||:|
DB      1 AKLVKKL 7

RESULT 48
US-11-303-372-83
; Sequence 83, Application US/11303372
; Publication No. US20060100149A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: D form peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: D form retroinversion peptide
US-11-303-372-83

Query Match      27.8%; Score 20; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 VPSVAKSVK 10
       |||:|
DB      6 VPLVVAARK 15

RESULT 49
US-11-303-372-84
; Sequence 84, Application US/11303372
; Publication No. US20060100149A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: D form retroinversion peptide
US-11-303-372-84

Query Match      27.8%; Score 20; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 VPSVAKSVK 10
       |||:|
DB      6 VPLVVAARK 15

RESULT 50
US-11-061-841-310
; Sequence 310, Application US/11061841
; Publication No. US20060122377A1
; GENERAL INFORMATION:
; APPLICANT: DENNIS, MARK S.
; TITLE OF INVENTION: CDR-REPAIRED ANTIBODIES
; FILE REFERENCE: P2070R1
; CURRENT APPLICATION NUMBER: US/11/061,841
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US 60/545,840
; PRIOR FILING DATE: 2004-02-19
```

```
; NUMBER OF SEQ ID NOS: 441
; SEQ ID NO 310
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-061-841-310

Query Match          26.4%; Score 19; DB 7; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          11 LVLG 15
           |||
           2 SYLG 6

Db

RESULT 51
US-11-140-487A-79
; Sequence 79, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C virus
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-79

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          12 LVLG 15
           |||
           2 LVLG 5

Db

RESULT 52
US-11-140-487A-175
; Sequence 175, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C virus
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
```

```
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 175
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-175

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          12 LVLG 15
           |||
           2 LVLG 5

Db

RESULT 53
US-11-140-487A-319
; Sequence 319, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C virus
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 319
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-319

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          12 LVLG 15
           |||
           2 LVLG 5

Db

RESULT 54
US-11-140-487A-428
; Sequence 428, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C virus
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
```

```

; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-428
```

```

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 LYL6 15
       ||:|
Db      3 LYG 6
```

```

RESULT 55
US-11-140-487A-580
; Sequence 580, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 580
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-580
```

```

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 LYL6 15
       ||:|
Db      4 LYG 7
```

```

RESULT 56
US-11-140-487A-584
; Sequence 584, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
```

```

; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 584
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-584
```

```

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 LYL6 15
       ||:|
Db      2 LYG 5
```

```

RESULT 57
US-11-140-487A-638
; Sequence 638, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 638
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-638
```

```

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      12 LYL6 15
       ||:|
Db      3 LYG 6
```

```

RESULT 58
```


US-11-140-487A-745
; Sequence 745, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 745
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-745

Query Match 26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LYLIG 15
Db 3 LYLIG 6

RESULT 59
US-11-140-487A-1320
; Sequence 1320, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1320
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1320

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSVKSL 12

Db 1 KEVRSL 6

RESULT 60
US-11-140-487A-1670
; Sequence 1670, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1670

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LYLIG 15
Db 2 LYLIG 5

RESULT 61
US-11-140-487A-1702
; Sequence 1702, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1702
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1702

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSVKSL 12

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVLG 15
|:|:|
Db 7 LVIG 10

RESULT 62
US-11-140-487A-1820
; Sequence 1820, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1820
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1820

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVLG 15
|:|:|
Db 4 LVIG 7

RESULT 63
US-11-134-871-325
; Sequence 325, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-325

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAK 7
|:|:|
Db 3 VNFNVSK 9

RESULT 64
US-10-953-613C-409
; Sequence 409, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion,
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINSE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 409
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-409

Query Match 26.4%; Score 19; DB 6; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|
Db 6 PYSVQR 11

RESULT 65
US-10-953-613C-119
; Sequence 119, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINSE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 119
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-119

Query Match 26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|
Db 7 PYSVQR 12

RESULT 66
US-10-953-613C-123
; Sequence 123, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nesspor, Thomas

```

; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 123
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-123

Query Match
Best Local Similarity 26.4%; Score 19; DB 6; Length 12;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAK 7
Db 7 PYSVQR 12

RESULT 67
US-10-953-613C-127
; Sequence 127, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 127
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-127

Query Match
Best Local Similarity 26.4%; Score 19; DB 6; Length 12;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAK 7
Db 7 PYSVQR 12

RESULT 68
US-10-953-613C-131
; Sequence 131, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 131
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-131
```

```

Query Match
Best Local Similarity 26.4%; Score 19; DB 6; Length 12;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAK 7
Db 7 PYSVQR 12

RESULT 69
US-10-953-613C-139
; Sequence 139, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 139
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-139

Query Match
Best Local Similarity 26.4%; Score 19; DB 6; Length 12;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAK 7
Db 7 PYSVQR 12

RESULT 70
US-10-953-613C-140
; Sequence 140, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 140
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-140

Query Match
Best Local Similarity 26.4%; Score 19; DB 6; Length 12;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAK 7
Db 7 PYSVQR 12

RESULT 71
US-10-953-613C-141
; Sequence 141, Application US/10953613C
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```
RESULT 76
US-10-953-613C-147
; Sequence 147, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 147
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-147

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 77
US-10-953-613C-148
; Sequence 148, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 148
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-148

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 78
US-10-953-613C-149
; Sequence 149, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
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; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 149
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-149

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 79
US-10-953-613C-150
; Sequence 150, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 150
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-150

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 80
US-10-953-613C-151
; Sequence 151, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 151
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-151

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Oy	2	PRSVAK	7
	:	:	:
Db	7	PYSVQR	12

Search completed: July 12, 2006, 05:54:34
Job time : 28 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:30:20 ; Search time 192 Seconds
(without alignments)
35.720 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYIG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

Database :

A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	72	100.0	15	9	ADV91451 Human gro
2	36	50.0	12	2	AAV17975 Peptide S
3	30	41.7	12	9	ADW47130 Anti-CD20
4	30	41.7	12	9	AEA46220 Apolipop
5	29	40.3	9	9	ADW12121 Human CD2
6	29	40.3	10	8	ADK40054 PNA.molec
7	28	38.9	7	8	ADU08556 Heat shoc
8	28	38.9	8	8	ADU08552s Novel hyd
9	28	38.9	8	8	ADU08445 Heat shoc
10	28	38.9	8	8	ADU08841 Heat shoc
11	28	38.9	9	8	ADT73328 Human RSV
12	28	38.9	11	4	AAE00650 Alpha-1,2
13	28	38.9	11	4	AAE00650 Alpha-1,2
14	28	38.9	15	4	AAE97744 gp100 der
15	28	38.9	15	4	AAE97744 gp100 der
16	28	38.9	15	4	AAE98135 Interfero
17	28	38.9	15	4	AAE98135 Interfero
18	28	38.9	15	6	ABP73086 Anti aci
19	28	38.9	15	6	ABR31599 Human can
20	28	38.9	15	6	ABR31599 Human can
21	28	38.9	15	6	ABR31599 Human can
22	28	38.9	15	6	ABR31599 Human can
23	28	38.9	15	6	ABR31599 Human can

24	28	38.9	15	8	ADN71829 Human 273
25	28	38.9	15	8	ADN71169 Human 273
26	28	38.9	15	8	ADN71392 Human 273
27	28	38.9	15	8	ADN70835 Human 273
28	27.5	38.2	14	5	AAV59641 HIV rep11
29	27.5	38.2	14	5	AAV97491 Human imm
30	27	37.5	11	8	AD144462 C. dactyl
31	27	37.5	11	9	ABE28067 Cynodon d
32	27	37.5	11	9	ABE13465 Cynodon d
33	27	37.5	12	2	ADW47132 Anti-CD20
34	27	37.5	15	4	AAE64140 Ribosomal
35	27	37.5	15	7	ADG73517 E faecali
36	27	37.5	15	9	ADV22635 HIV-1 Rev
37	27	37.5	15	9	AECl1117 Enterococ
38	26	36.1	9	8	ADT73299 Human RSV
39	26	36.1	9	8	ADT73299 Human RSV
40	26	36.1	10	8	ADK40048 PNA molec
41	26	36.1	11	6	ABJ36740 G protein
42	26	36.1	11	8	ADT51155 G protein
43	26	36.1	12	2	AAE68663 T cell ep
44	26	36.1	12	2	AAW25833 HIV B-cel
45	26	36.1	12	2	AAE67349 HIV-1 str
46	26	36.1	12	2	AAW99957 HIV-1 vac
47	26	36.1	12	2	AAV39755 HIV1 chim
48	26	36.1	12	5	AAU70355 Mouse Kap
49	26	36.1	12	8	ADBE2804 Anti-alph
50	26	36.1	12	8	ADH59661 Light cha
51	26	36.1	12	8	ADH59682 Light cha
52	26	36.1	14	7	ADD90504 Novel hum
53	26	36.1	14	7	ADD90323 Human sec
54	26	36.1	14	9	ADU83344 Nkappa B
55	26	36.1	14	9	ADY25663 Novel hum
56	26	36.1	14	9	AE36996 Novel lam
57	26	36.1	14	9	AE318167 Prion dis
58	26	36.1	15	2	AAW12084 T-cell ep
59	26	36.1	15	2	AAW11956 T-cell ep
60	26	36.1	15	2	AAW12086 T-cell ep
61	26	36.1	15	2	AAW12085 T-cell ep
62	26	36.1	15	2	AAW12083 T-cell ep
63	26	36.1	15	2	AAW08008 V3 peptid
64	26	36.1	15	5	ABP30990 Peptide #
65	26	36.1	15	5	ABP56426 Human sco
66	26	36.1	15	7	ADAO8653 Human O77
67	26	36.1	15	7	ADP08996 Secreted
68	26	36.1	15	8	ADN94643 Human 202
69	26	36.1	15	8	ADN94644 Human 202
70	26	36.1	15	8	ADN94062 Human 202
71	26	36.1	15	8	ADN94078 Human 202
72	26	36.1	15	9	ADX17879 Human ova
73	25.5	35.4	14	8	ADM19018 HLA-DR bo
74	25.5	35.4	15	8	ADM19019 HLA-DR bo
75	25	34.7	8	3	AAV77393 HIV-1 gro
76	25	34.7	8	5	ABE76741 Tumour an
77	25	34.7	8	8	ADH62104 Cyclic an
78	25	34.7	8	8	ADP67919 Anti-micr
79	25	34.7	8	8	ADOC28132 Exclud
80	25	34.7	9	2	AAE84828 Modified
81	25	34.7	9	2	AAE84831 Modified
82	25	34.7	9	2	AAE84210 Modified
83	25	34.7	9	2	AAE84821 Modified
84	25	34.7	9	2	AAE84827 Modified
85	25	34.7	9	2	AAE84832 Modified
86	25	34.7	9	2	AAE84833 Modified
87	25	34.7	9	2	AAE84829 Modified
88	25	34.7	9	2	AAE84822 Modified
89	25	34.7	9	2	AAE84830 Modified
90	25	34.7	9	2	AAE84834 Modified
91	25	34.7	9	2	AAE84820 Modified
92	25	34.7	9	2	AAE84823 Modified
93	25	34.7	9	2	AAE84816 Modified
94	25	34.7	9	2	AAE84817 Modified
95	25	34.7	9	2	AAE84824 Modified
96	25	34.7	9	2	AAE84825 Modified

97	25	34.7	9	2	AAE84826	AAE84826 Modified	170	25	34.7	9	5	ABG79042	ABG79042 Human Gp1
98	25	34.7	9	2	AAE84835	AAE84835 Modified	171	25	34.7	9	5	AAO17085	AAO17085 Gp 100 an
99	25	34.7	9	2	AAE84818	AAE84818 Modified	172	25	34.7	9	5	AAO18865	AAO18865 Human gp1
100	25	34.7	9	2	AAE84819	AAE84819 Modified	173	25	34.7	9	5	AAE26788	AAE26788 Human gp1
101	25	34.7	9	2	AAE84836	AAE84836 Modified	174	25	34.7	9	5	AAU09706	AAU09706 Human gp1
102	25	34.7	9	2	AAW70018	AAW70018 Modified	175	25	34.7	9	5	AAU09696	AAU09696 Human gp1
103	25	34.7	9	2	AAW71117	AAW71117 Modified	176	25	34.7	9	5	ABG66780	ABG66780 Human gp1
104	25	34.7	9	2	AAW54599	AAW54599 Modified	177	25	34.7	9	5	ABG60131	ABG60131 Human gp1
105	25	34.7	9	2	AAW78851	AAW78851 Modified	178	25	34.7	9	5	AAE17297	AAE17297 Human gp1
106	25	34.7	9	2	AAW71210	AAW71210 Modified	179	25	34.7	9	5	AAE36294	AAE36294 Human gp1
107	25	34.7	9	2	AAV10448	AAV10448 Modified	180	25	34.7	9	6	AAE36055	AAE36055 Human gp1
108	25	34.7	9	2	AAV40214	AAV40214 Modified	181	25	34.7	9	6	AAE36055	AAE36055 Human gp1
109	25	34.7	9	2	AAV47617	AAV47617 Modified	182	25	34.7	9	6	AAE36055	AAE36055 Human gp1
110	25	34.7	9	2	AAV33173	AAV33173 Modified	183	25	34.7	9	6	AAE36055	AAE36055 Human gp1
111	25	34.7	9	2	AAV35527	AAV35527 Modified	184	25	34.7	9	6	AAE36055	AAE36055 Human gp1
112	25	34.7	9	2	AAV26870	AAV26870 Modified	185	25	34.7	9	6	AAE36055	AAE36055 Human gp1
113	25	34.7	9	2	AAV00716	AAV00716 Modified	186	25	34.7	9	6	AAE36055	AAE36055 Human gp1
114	25	34.7	9	2	AAV49654	AAV49654 Modified	187	25	34.7	9	6	AAE36055	AAE36055 Human gp1
115	25	34.7	9	2	AAV01754	AAV01754 Modified	188	25	34.7	9	6	AAE36055	AAE36055 Human gp1
116	25	34.7	9	2	AAV15121	AAV15121 Modified	189	25	34.7	9	6	AAE36055	AAE36055 Human gp1
117	25	34.7	9	3	AAV90804	AAV90804 Modified	190	25	34.7	9	6	AAE36055	AAE36055 Human gp1
118	25	34.7	9	3	AAV84766	AAV84766 Modified	191	25	34.7	9	6	AAE36055	AAE36055 Human gp1
119	25	34.7	9	3	AAV84770	AAV84770 Modified	192	25	34.7	9	6	AAE36055	AAE36055 Human gp1
120	25	34.7	9	3	AAV83663	AAV83663 Modified	193	25	34.7	9	7	AAE36055	AAE36055 Human gp1
121	25	34.7	9	3	AAE23680	AAE23680 Modified	194	25	34.7	9	7	AAE36055	AAE36055 Human gp1
122	25	34.7	9	3	AAV92300	AAV92300 Modified	195	25	34.7	9	7	AAE36055	AAE36055 Human gp1
123	25	34.7	9	3	AAV56615	AAV56615 Modified	196	25	34.7	9	7	AAE36055	AAE36055 Human gp1
124	25	34.7	9	3	AAV84297	AAV84297 Modified	197	25	34.7	9	7	AAE36055	AAE36055 Human gp1
125	25	34.7	9	3	AAV82980	AAV82980 Modified	198	25	34.7	9	7	AAE36055	AAE36055 Human gp1
126	25	34.7	9	3	AAE02653	AAE02653 Modified	199	25	34.7	9	7	AAE36055	AAE36055 Human gp1
127	25	34.7	9	3	AAE08655	AAE08655 Modified	200	25	34.7	9	7	AAE36055	AAE36055 Human gp1
128	25	34.7	9	3	AAE02112	AAE02112 Modified	201	25	34.7	9	7	AAE36055	AAE36055 Human gp1
129	25	34.7	9	4	AAE95909	AAE95909 Modified	202	25	34.7	9	7	AAE36055	AAE36055 Human gp1
130	25	34.7	9	4	AAE93759	AAE93759 Modified	203	25	34.7	9	7	AAE36055	AAE36055 Human gp1
131	25	34.7	9	4	AAE02662	AAE02662 Modified	204	25	34.7	9	7	AAE36055	AAE36055 Human gp1
132	25	34.7	9	4	AAU28973	AAU28973 Modified	205	25	34.7	9	7	AAE36055	AAE36055 Human gp1
133	25	34.7	9	4	AAU28974	AAU28974 Modified	206	25	34.7	9	7	AAE36055	AAE36055 Human gp1
134	25	34.7	9	4	AAU28965	AAU28965 Modified	207	25	34.7	9	7	AAE36055	AAE36055 Human gp1
135	25	34.7	9	4	AAU28976	AAU28976 Modified	208	25	34.7	9	7	AAE36055	AAE36055 Human gp1
136	25	34.7	9	4	AAU28970	AAU28970 Modified	209	25	34.7	9	7	AAE36055	AAE36055 Human gp1
137	25	34.7	9	4	AAU28972	AAU28972 Modified	210	25	34.7	9	7	AAE36055	AAE36055 Human gp1
138	25	34.7	9	4	AAU28977	AAU28977 Modified	211	25	34.7	9	7	AAE36055	AAE36055 Human gp1
139	25	34.7	9	4	AAU28983	AAU28983 Modified	212	25	34.7	9	7	AAE36055	AAE36055 Human gp1
140	25	34.7	9	4	AAU28968	AAU28968 Modified	213	25	34.7	9	7	AAE36055	AAE36055 Human gp1
141	25	34.7	9	4	AAU28978	AAU28978 Modified	214	25	34.7	9	7	AAE36055	AAE36055 Human gp1
142	25	34.7	9	4	AAU28981	AAU28981 Modified	215	25	34.7	9	7	AAE36055	AAE36055 Human gp1
143	25	34.7	9	4	AAU28984	AAU28984 Modified	216	25	34.7	9	7	AAE36055	AAE36055 Human gp1
144	25	34.7	9	4	AAU28979	AAU28979 Modified	217	25	34.7	9	7	AAE36055	AAE36055 Human gp1
145	25	34.7	9	4	AAU28985	AAU28985 Modified	218	25	34.7	9	7	AAE36055	AAE36055 Human gp1
146	25	34.7	9	4	AAU28971	AAU28971 Modified	219	25	34.7	9	7	AAE36055	AAE36055 Human gp1
147	25	34.7	9	4	AAU28960	AAU28960 Modified	220	25	34.7	9	7	AAE36055	AAE36055 Human gp1
148	25	34.7	9	4	AAU28930	AAU28930 Modified	221	25	34.7	9	7	AAE36055	AAE36055 Human gp1
149	25	34.7	9	4	AAU28967	AAU28967 Modified	222	25	34.7	9	7	AAE36055	AAE36055 Human gp1
150	25	34.7	9	4	AAU28975	AAU28975 Modified	223	25	34.7	9	7	AAE36055	AAE36055 Human gp1
151	25	34.7	9	4	AAU28966	AAU28966 Modified	224	25	34.7	9	7	AAE36055	AAE36055 Human gp1
152	25	34.7	9	4	AAU28969	AAU28969 Modified	225	25	34.7	9	7	AAE36055	AAE36055 Human gp1
153	25	34.7	9	4	AAU28962	AAU28962 Modified	226	25	34.7	9	7	AAE36055	AAE36055 Human gp1
154	25	34.7	9	4	AAU28932	AAU28932 Modified	227	25	34.7	9	7	AAE36055	AAE36055 Human gp1
155	25	34.7	9	4	AAU28954	AAU28954 Modified	228	25	34.7	9	7	AAE36055	AAE36055 Human gp1
156	25	34.7	9	4	AAU28958	AAU28958 Modified	229	25	34.7	9	7	AAE36055	AAE36055 Human gp1
157	25	34.7	9	4	AAU28953	AAU28953 Modified	230	25	34.7	9	7	AAE36055	AAE36055 Human gp1
158	25	34.7	9	4	AAU28959	AAU28959 Modified	231	25	34.7	9	7	AAE36055	AAE36055 Human gp1
159	25	34.7	9	4	AAU28955	AAU28955 Modified	232	25	34.7	9	7	AAE36055	AAE36055 Human gp1
160	25	34.7	9	4	AAU28956	AAU28956 Modified	233	25	34.7	9	7	AAE36055	AAE36055 Human gp1
161	25	34.7	9	4	AAU28957	AAU28957 Modified	234	25	34.7	9	7	AAE36055	AAE36055 Human gp1
162	25	34.7	9	4	AAU28958	AAU28958 Modified	235	25	34.7	9	7	AAE36055	AAE36055 Human gp1
163	25	34.7	9	4	AAU28959	AAU28959 Modified	236	25	34.7	9	7	AAE36055	AAE36055 Human gp1
164	25	34.7	9	4	AAU28960	AAU28960 Modified	237	25	34.7	9	7	AAE36055	AAE36055 Human gp1
165	25	34.7	9	4	AAU28961	AAU28961 Modified	238	25	34.7	9	7	AAE36055	AAE36055 Human gp1
166	25	34.7	9	4	AAU28962	AAU28962 Modified	239	25	34.7	9	7	AAE36055	AAE36055 Human gp1
167	25	34.7	9	4	AAU28963	AAU28963 Modified	240	25	34.7	9	7	AAE36055	AAE36055 Human gp1
168	25	34.7	9	4	AAU28964	AAU28964 Modified	241	25	34.7	9	7	AAE36055	AAE36055 Human gp1
169	25	34.7	9	4	AAU28965	AAU28965 Modified	242	25	34.7	9	7	AAE36055	AAE36055 Human gp1

243	25	34.7	9	8	AD043392	Ad043392 Human tum	316	25	34.7	15	6	ABR37165	Ab37165 Human can
244	25	34.7	9	8	AD010868	Ad010868 Homo sapi	317	25	34.7	15	6	ABR36781	Ab36781 Human can
245	25	34.7	9	8	AD087048	Ad087048 Human gen	318	25	34.7	15	6	ABR37398	Ab37398 Human can
246	25	34.7	9	8	ADRC9741	AdRC9741 Novel1 hyd	319	25	34.7	15	6	ABR00910	Ab00910 Bioactive
247	25	34.7	9	8	ADSS2359	AdSS2359 HLA-A2 re	320	25	34.7	15	8	ADN71198	Adn71198 Human 273
248	25	34.7	9	8	AD575029	Ad575029 Human mel	321	25	34.7	15	8	ADN71619	Adn71619 Human 273
249	25	34.7	9	8	ADSS81348	AdSS81348 Tumour-as	322	25	34.7	15	9	ADV22141	Adv22141 SHIV env
250	25	34.7	9	8	ADT73579	AdT73579 Human RSV	323	25	34.7	15	9	ADW78280	Adw78280 Mouse neu
251	25	34.7	9	8	ADT73578	AdT73578 Human RSV	324	25	34.7	15	9	ADW78288	Adw78288 Rat DEF d
252	25	34.7	9	8	ADT25862	AdT25862 Human mel	325	25	34.7	15	10	AE66548	Ae66548 Peptide f
253	25	34.7	9	8	ADU08482	AdU08482 Cancer an	326	25	34.7	7	5	ABP67285	Abp67285 Human CD6
254	25	34.7	9	8	ADU08497	AdU08497 IMD_Pepti	327	25	34.7	8	2	AA1Y16811	Aa1Y16811 Heat choc
255	25	34.7	9	8	ADU87382	AdU87382 Human mel	328	25	34.7	8	5	ABP67278	Abp67278 Human CD6
256	25	34.7	9	9	ADU69291	AdU69291 HIV-1 gp1	329	25	34.7	8	5	ADP67279	Adp67279 Human CD6
257	25	34.7	9	9	ADW13784	AdW13784 Human mel	330	25	34.7	8	7	ADG72881	Adg72881 Heat choc
258	25	34.7	9	9	ADW12146	AdW12146 Human CD2	331	25	34.7	8	8	ADK09058	Adk09058 Human pap
259	25	34.7	9	9	ADX08558	AdX08558 Class I H	332	25	34.7	8	8	ADU08595	AdU08595 Heat choc
260	25	34.7	9	9	ADY26211	AdY26211 MHC Class	333	25	34.7	8	9	ADV34214	Adv34214 Consensus
261	25	34.7	9	9	ADZ00248	AdZ00248 Cancer im	334	25	34.7	9	3	AA080572	Aa080572 Peptide i
262	25	34.7	9	9	ADZ67829	AdZ67829 Majdr his	335	25	34.7	9	5	AAE28752	Aae28752 Human CAS
263	25	34.7	9	9	AE828684	Ae828684 Human leu	336	25	34.7	9	5	ABP67273	Abp67273 Human CD6
264	25	34.7	9	9	AEC92213	Aec92213 Melanoma	337	25	34.7	9	5	ABP67274	Abp67274 Human CD6
265	25	34.7	9	9	AEC92214	Aec92214 Melanoma	338	25	34.7	9	6	ABP75230	Abp75230 Chlamydia
266	25	34.7	9	9	AED14746	Aed14746 Peptide f	339	25	34.7	9	6	ABR04765	Ab04765 Human can
267	25	34.7	9	10	AEE91627	Aee91627 HLA-A0201	340	25	34.7	9	6	ABR05751	Ab05751 Human can
268	25	34.7	9	10	AEF01170	Aef01170 Melanocyte	341	25	34.7	9	6	ABR05919	Ab05919 Human can
269	25	34.7	10	2	AAW29931	Aaw29931 Rat isp. A	342	25	34.7	9	6	ABR24011	Ab24011 Human can
270	25	34.7	10	2	AAW29915	Aaw29915 Porcine A	343	25	34.7	9	6	ABR23820	Ab23820 Human can
271	25	34.7	10	2	AA1Y10450	Aa1Y10450 HLA Class	344	25	34.7	9	6	ABR05106	Ab05106 Human can
272	25	34.7	10	4	AAU28931	Aau28931 gp100 Imm	345	25	34.7	9	6	ABR04896	Ab04896 Human can
273	25	34.7	10	4	AAU71990	Aau71990 gp100 mel	346	25	34.7	9	6	ABR05876	Ab05876 Human can
274	25	34.7	10	4	AAAG94017	Aaag94017 Human com	347	25	34.7	9	6	ADN68721	Adn68721 Human 273
275	25	34.7	10	4	AAAG861348	Aaag861348 Saccharom	348	25	34.7	9	8	ADN68721	Adn68721 Human 273
276	25	34.7	10	5	ABG80133	Abg80133 MHC Class	349	25	34.7	9	8	ADN67589	Adn67589 Human 273
277	25	34.7	10	6	ABR05642	Ab05642 Human can	350	25	34.7	9	8	ADN67344	Adn67344 Human 273
278	25	34.7	10	6	ABR06013	Ab06013 Human can	351	25	34.7	9	8	ADN69490	Adn69490 Human 273
279	25	34.7	10	6	ABR91263	Ab91263 P. papata	352	25	34.7	10	3	AA1Y81466	Aa1Y81466 E. coli "
280	25	34.7	10	7	ADB97698	Adb97698 Human mel	353	25	34.7	10	4	AAAG95531	Aaag95531 Human com
281	25	34.7	10	8	ADK40049	Adk40049 PNA'molec	354	25	34.7	10	4	AAAG42903	Aaag42903 Mycoplasma
282	25	34.7	10	8	ADK69072	Adk69072 Eptlope 1	355	25	34.7	10	4	AAAG43172	Aaag43172 Mycoplasma
283	25	34.7	10	8	ADN91507	Adn91507 Human 202	356	25	34.7	10	5	ABBS1836	Abbs1836 Human 34P
284	25	34.7	10	8	ADN93796	Adn93796 Human 202	357	25	34.7	10	5	ABBS1606	Abbs1606 Human 34P
285	25	34.7	10	8	ADN93977	Adn93977 Human 202	358	25	34.7	10	5	ABBS1536	Abbs1536 Human 34P
286	25	34.7	10	8	ADN93487	Adn93487 Human 202	359	25	34.7	10	5	ABBS1906	Abbs1906 Human 34P
287	25	34.7	10	8	ADN90273	Adn90273 Human 202	360	25	34.7	10	5	ABP67269	Abp67269 Human CD6
288	25	34.7	10	8	ADN91212	Adn91212 Human 202	361	25	34.7	10	5	ABP67270	Abp67270 Human CD6
289	25	34.7	10	8	ADN91830	Adn91830 Human 202	362	25	34.7	10	6	ABR06022	Ab06022 Human can
290	25	34.7	10	8	ADN93858	Adn93858 Human 202	363	25	34.7	10	6	ABR24316	Ab24316 Human can
291	25	34.7	10	8	ADQ10870	Adq10870 Homo sapi	364	25	34.7	10	6	ABR24316	Ab24316 Human can
292	25	34.7	10	8	ADSS81350	AdSS81350 Tumour-as	365	25	34.7	10	6	ABR23958	Ab23958 Human can
293	25	34.7	11	2	AAW23266	Aaw23266 Tumour ne	366	25	34.7	10	6	ABR24126	Ab24126 Human can
294	25	34.7	11	6	ABR91265	Ab91265 P. papata	367	25	34.7	10	6	ABR05252	Ab05252 Human can
295	25	34.7	12	5	ABP67265	Abp67265 Human CD6	368	25	34.7	10	6	ABR05620	Ab05620 Human can
296	25	34.7	12	8	AD042769	Ad042769 Leader se	369	25	34.7	10	6	ABR05843	Ab05843 Human can
297	25	34.7	13	4	AAAB88001	AaAB88001 CD66 pep	370	25	34.7	10	6	ABR06035	Ab06035 Human can
298	25	34.7	13	5	ABP67241	Abp67241 Human CD6	371	25	34.7	10	6	ABR05783	Ab05783 Human can
299	25	34.7	13	8	ADG78907	Adg78907 Control p	372	25	34.7	10	6	ABR05652	Ab05652 Human can
300	25	34.7	13	8	ADN48981	Adn48981 Control p	373	25	34.7	10	6	ABR05853	Ab05853 Human can
301	25	34.7	13	9	AED80661	Aed80661 PNC-29 co	374	25	34.7	11	5	ADN67806	Adn67806 Human 273
302	25	34.7	14	2	AAAR05280	AaAR05280 Human int	375	25	34.7	10	8	ADN70212	Adn70212 Human 273
303	25	34.7	15	1	AAAP90266	AaAP90266 Antigenic	376	25	34.7	10	8	ADN67782	Adn67782 Human 273
304	25	34.7	15	2	AAAR94865	AaAR94865 Peptide f	377	25	34.7	10	8	ADP25590	Adp25590 Plasmodiu
305	25	34.7	15	2	AAAW43543	AaAW43543 Mycobacte	378	25	34.7	10	8	ADR10571	Adr10571 Penicilliu
306	25	34.7	15	2	AA1Y21511	Aa1Y21511 Human neu	379	25	34.7	11	5	ABP67268	Abp67268 Human CD6
307	25	34.7	15	4	ABP24463	Abp24463 HIV DR su	380	25	34.7	11	5	ABP67267	Abp67267 Human CD6
308	25	34.7	15	5	AAO15130	AaO15130 Human pot	381	25	34.7	11	5	ABP67266	Abp67266 Human CD6
309	25	34.7	15	6	ABR31541	Ab31541 Human can	382	25	34.7	11	6	ABR00885	Ab00885 Bioactive
310	25	34.7	15	6	ABR30594	Ab30594 Human can	383	25	34.7	12	2	AAAR42324	AaAR42324 EBV VCA p
311	25	34.7	15	6	ABR36884	Ab36884 Human can	384	25	34.7	12	2	AAAR42323	AaAR42323 EBV VCA p
312	25	34.7	15	6	ABR37666	Ab37666 Human can	385	25	34.7	12	5	ABP67264	Abp67264 Human CD6
313	25	34.7	15	6	ABR37751	Ab37751 Human can	386	25	34.7	12	5	ADW47131	Adw47131 Anti-CD20
314	25	34.7	15	6	ABR37259	Ab37259 Human can	387	25	34.7	12	9	ADX18723	Adx18723 Novel kin
315	25	34.7	15	6	ABR30841	Ab30841 Human can	388	25	34.7	12	9	ADX18773	Adx18773 Novel kin

681	23	31.9	14	4	AAB92233	Aab92233 Toxin pep
682	23	31.9	14	4	AAB88163	Aab88163 CD66 pep
683	23	31.9	14	6	ADA19583	Ada19583 Carcinoem
684	23	31.9	14	8	ADU48708	Adu48708 Human int
685	23	31.9	14	9	AED80969	Aed80969 Vespa ori
686	23	31.9	15	1	AAP82830	Aap82830 Non-A, NO
687	23	31.9	15	2	AAR14336	Aar14336 Sciavo pe
688	23	31.9	15	2	AAR14397	Aar14397 Sciavo pe
689	23	31.9	15	2	AAR62572	Aar62572 Human hep
690	23	31.9	15	2	AAM29479	Aam29479 Peptide e
691	23	31.9	15	2	AAM29487	Aam29487 Peptide #
692	23	31.9	15	2	AAW73220	Aaw73220 Histone H
693	23	31.9	15	2	AAW73425	Aaw73425 Human sec
694	23	31.9	15	2	AAW57349	Aaw57349 Human his
695	23	31.9	15	3	AAV65813	Aav65813 FADD-homo
696	23	31.9	15	4	ABBI2911	Abbi2911 Human C35
697	23	31.9	15	4	ABBI2870	Abbi2870 Human C35
698	23	31.9	15	4	ABBI2831	Abbi2831 Human C35
699	23	31.9	15	4	ABBI2923	Abbi2923 Human C35
700	23	31.9	15	4	AAV64562	Aav64562 Human myo
701	23	31.9	15	4	ABP24487	Abp24487 HIV DR su
702	23	31.9	15	4	ABP24431	Abp24431 HIV DR su
703	23	31.9	15	5	ABP58713	Abp58713 Human fib
704	23	31.9	15	5	ABP58729	Abp58729 Rhodopsin
705	23	31.9	15	6	ABR33632	Abri33632 Human can
706	23	31.9	15	6	ABR33656	Abri33656 Human can
707	23	31.9	15	6	ABR33718	Abri33718 Human can
708	23	31.9	15	6	ABR33684	Abri33684 Human can
709	23	31.9	15	6	ABR33746	Abri33746 Human can
710	23	31.9	15	6	ABR33668	Abri33668 Human can
711	23	31.9	15	6	ABR33765	Abri33765 Human can
712	23	31.9	15	6	ABR33619	Abri33619 Human can
713	23	31.9	15	6	ABR33766	Abri33766 Human can
714	23	31.9	15	7	ADC54047	Adc54047 Human reg
715	23	31.9	15	7	ADL00354	Adl00354 Polypept
716	23	31.9	15	8	ADL14271	Adl14271 Immunogen
717	23	31.9	15	8	ADN71512	Adn71512 Human 273
718	23	31.9	15	8	ADN70546	Adn70546 Human 273
719	23	31.9	15	8	ADN65099	Adn65099 HLA bindi
720	23	31.9	15	8	ADN65098	Adn65098 HLA bindi
721	23	31.9	15	8	ADN65110	Adn65110 HLA bindi
722	23	31.9	15	8	ADN65280	Adn65280 HLA bindi
723	23	31.9	15	8	ADN05702	Adn05702 Antipsofi
724	23	31.9	15	8	AD047146	Ado47146 Antio aci
725	23	31.9	15	8	ADP26479	Adp26479 Plasmodu
726	23	31.9	15	8	AD513553	Ad513553 Human rbe
727	23	31.9	15	8	ADT07826	Adt07826 Human int
728	23	31.9	15	8	ADM15936	Adm15936 Human act
729	23	31.9	15	9	ADV44318	Adv44318 Human Hdm
730	23	31.9	15	9	ADV91487	Adv91487 Human Gas
731	23	31.9	15	9	ADV21599	Adv21599 SIV gag p
732	23	31.9	15	9	ADV22686	Adv22686 HIV-1 Vif
733	23	31.9	15	9	ADV70545	Adv70545 Bovine pa
734	23	31.9	15	9	ADM12731	Adm12731 HIV-1 gp1
735	23	31.9	15	9	ADY71996	Ady71996 Human Imm
736	23	31.9	15	9	ADZ69811	Adz69811 Botulinum
737	23	31.9	15	9	ADZ69739	Adz69739 Botulinum
738	23	31.9	15	9	ADZ69754	Adz69754 Botulinum
739	23	31.9	15	9	AEC23563	Aec23563 Human c-S
740	23	31.9	15	9	AEC98732	Aec98732 HLA-DR bi
741	23	31.9	15	9	AEC98731	Aec98731 HLA-DR bi
742	23	31.9	15	9	AEC98731	Aec98731 HLA-DR bi
743	23	31.9	15	9	ABP67301	Abp67301 Human CD6
744	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
745	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
746	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
747	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
748	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
749	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
750	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
751	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
752	23	31.9	15	9	ADJ82667	Adj82667 Shuffled
753	23	31.9	15	9	ADJ82667	Adj82667 Shuffled

754	22	30.6	8	9	AEC11479	Aec11479 Enterococ
755	22	30.6	9	2	AAR89370	Aar89370 Cw6 conse
756	22	30.6	9	4	AAU27018	Aau27018 Human Leu
757	22	30.6	9	4	AAU26685	Aau26685 Human Leu
758	22	30.6	9	4	ABP11572	Abp11572 HIV A01 s
759	22	30.6	9	4	ABP15318	Abp15318 HIV A24 s
760	22	30.6	9	4	ABP18459	Abp18459 HIV B62 s
761	22	30.6	9	6	ABU08168	Abu08168 MART-1 57
762	22	30.6	9	7	ADM33074	Adm33074 Human tum
763	22	30.6	9	7	ADM33074	Adm33074 Human tum
764	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
765	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
766	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
767	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
768	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
769	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
770	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
771	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
772	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
773	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
774	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
775	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
776	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
777	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
778	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
779	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
780	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
781	22	30.6	9	8	ADP25786	Adp25786 Plasmodu
782	22	30.6	9	10	AEE63125	Aee63125 ML-TAP (1
783	22	30.6	10	3	ABP13857	Abp13857 Influenza
784	22	30.6	10	4	ABP14114	Abp14114 Human C35
785	22	30.6	10	4	ABP17615	Abp17615 HIV B58 s
786	22	30.6	10	4	ABP11596	Abp11596 HIV A01 s
787	22	30.6	10	5	AAU10525	Aau10525 Human leu
788	22	30.6	10	6	ABR05416	Abri05416 Human can
789	22	30.6	10	7	ADP91942	Adp91942 P. papara
790	22	30.6	10	7	ADA49582	Ada49582 Multi-epi
791	22	30.6	10	8	ADK40055	Adk40055 PNA molec
792	22	30.6	10	8	ADK40051	Adk40051 PNA molec
793	22	30.6	10	8	ADK40044	Adk40044 PNA molec
794	22	30.6	10	8	ADK40044	Adk40044 PNA molec
795	22	30.6	10	8	ADM72002	Adm72002 Tumour an
796	22	30.6	10	8	ADM71339	Adm71339 Chemokine
797	22	30.6	10	8	ADM71339	Adm71339 Chemokine
798	22	30.6	10	9	ADO24260	Ado24260 P falcipa
799	22	30.6	10	9	ADC240762	Adc240762 Multi-epi
800	22	30.6	11	4	AAB72860	Aab72860 Human p53

ALIGNMENTS

RESULT 1	ADV91451	ADV91451 standard, peptide, 15 AA.
ID	ADV91451	
AC	ADV91451;	
DT	10-MAR-2005	(first entry)
DE	Human growth arrest specific gene 6 (Gase) G domain peptide #1.	
KW	Growth arrest specific gene 6; Gase6; cardiovascular disease; cancer;	
KW	atherosclerosis; sepsis; glomerulosclerosis; diabetes;	
KW	rheumatoid arthritis; HIV infection; osteoarthritis; osteoporosis;	
KW	multiple sclerosis; cardiovascular-gen.; antirheumatic; antiarthritic;	
KW	anti-HIV; cytostatic; neuroprotective; thrombolytic; cardian;	
KW	cerebroprotective; vasotropic; antidiabetic; osteopathic;	
KW	immunopressive; nephrotropic; antidiabetic; osteopathic;	
KW	antibody production.	
OS	Homo sapiens.	
XX		

PN	MO2004108748-A2.	
PD	16-DEC-2004.	
XX		
XX		
PF	24-SEP-2003; 2003WO-US029909.	
XX		
PR	24-SEP-2002; 2002US-0413250P.	
XX		
PA	(CENZ) CENTOCOR INC.	
XX		
PI	Yang J, Heavner G, Jordan R, Sweet RW;	
XX		
DR	WPI; 2005-031655/03.	
PT	Novel human growth arrest specific polypeptide-6, useful for generating	
PT	antibodies against growth arrest specific polypeptide-6, and for treating	
PT	cardiovascular, rheumatoid arthritis, HIV infection, leukemia, multiple	
PT	sclerosis.	
XX		
PS	Claim 1; SEQ ID NO 2; 107pp; English.	
XX		
CC	The invention relates to an isolated human growth arrest specific gene 6	
CC	(Gas6) polypeptide. The invention also relates to a recombinant DNA	
CC	molecule encoding the polypeptide, an antibody or antigen binding	
CC	fragment capable of binding to the polypeptide and a labeled antibody	
CC	generated against Gas6. The Gas6 polypeptide is useful for generating	
CC	antibodies against Gas6, which involves immunization with the polypeptide	
CC	or screening recombinant antibodies with the polypeptide. The antibodies	
CC	are useful for detecting Gas6 polypeptide in a sample suspected of	
CC	containing Gas6. Compositions containing the polypeptide are useful for	
CC	preventing or treating cardiovascular diseases resulting from a	
CC	dysfunction in a mammal. The compositions are also useful for treating	
CC	cancer, atherosclerosis, sepsis, glomerulosclerosis, diabetes, rheumatoid	
CC	arthritis, HIV infection, osteoarthritis, osteoporosis and multiple	
CC	sclerosis. This sequence represents a human Gas6 G domain peptide of the	
CC	invention.	
XX		
SO	Sequence 15 AA;	
	Query Match 100.0%; Score 72; DB 9; Length 15;	
	Best Local Similarity 100.0%; Pred. No. 5.5e-06;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 VPFSAKSVKSLYLIG 15	
	1 VPFSAKSVKSLYLIG 15	
DB		
RESULT 2		
	AA117975	
ID	AA117975 standard; peptide; 12 AA.	
XX		
AC	AA117975;	
XX		
CT	04-AUG-1999 (first entry)	
XX		
DE	Peptide Seq ID No: 6 of JP11127869.	
XX		
KW	Hexulose phosphate isomerase; enzyme; recombinant; M. gastri.	
XX		
OS	Mycobacterium gastri.	
XX		
PN	JP11127869-A.	
XX		
PD	18-MAY-1999.	
XX		
PF	09-JUL-1998; 98JP-00194808.	
XX		
PR	28-AUG-1997; 97JP-00233131.	
XX		
PA	(AJIN) AJINOMOTO KK.	
XX		
PI	Kato N;	

XX WP1; 1999-350329/30.
XX
XX New hexulose phosphate isomerase gene - prepared recombinantly with high
XX efficiency.
XX
XX Example; Page 6; 19pp; Japanese.
XX
XX The invention relates to a Mycobacterium gastrii hexulose phosphate
CC isomerase. The enzyme can be produced recombinantly by culturing a cell
CC which is transformed with a DNA coding for hexulose phosphate isomerase
CC and collecting the enzyme from the culture
XX
XX Sequence 12 AA;
SQ
Query Match 50.0%; Score 36; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 VPFSVAKSVK 10
||| ||| ||
3 VPFSVAGGVK 12 .
DB
RESULT 3
ADW47130
ID ADW47130 standard; peptide; 12 AA.
XX
XX ADW47130;
AC
XX
XX 24-MAR-2005 (first entry)
DT
XX
XX Anti-CD20 monoclonal antibody light chain MHB20-2,14 CDR 1.
DE
XX
XX CD20; monoclonal antibody; rheumatoid arthritis; antiarthritis;
KW antirheumatic; immune disorder; inflammation; musculoskeletal disease;
KW idiopathic thrombocytopenic purpura; hemostatic; hemolytic anemia.
XX
XX Mus musculus.
OS
XX
XX WO200500901-A2.
PN
XX
XX 06-JAN-2005.
PD
XX
XX 07-MAY-2004; 2004WO-US014326.
PF
XX
XX 09-MAY-2003; 2003US-0469451P.
PR
XX
XX (UYDU-) UNIV DUKE.
PA
XX
XX Tedder TF, Uchida J, Hamaguchi Y, Poe JC;
PI
XX
XX WP1; 2005-066556/07.
DR
XX
XX Novel monoclonal antibody (mAb) binding to CD20 or mouse CD20, in which
PT density of binding of mAb to B cells is two-fold higher than density of
PT binding of mAb to B cells, useful for depleting B cells, and treating
PT B cell disorder.
XX
XX Example 1; SEQ ID NO 89; 205pp; English.
PS
XX
XX The invention relates to a monoclonal antibody (mAb) or its antigen-
CC binding fragment that specifically binds to human CD20 or mouse CD20,
CC where the density of binding of mAb or antigen-binding fragment to B
CC cells is at least two-fold higher than the density of binding of mAb 1F5
CC to B cells. Also included are a pharmaceutical composition comprising mAb
CC in a carrier, a pharmaceutical composition (comprising mAb or its antigen
CC binding fragment which specifically binds to the same antigenic
CC determinant as a monoclonal antibody chosen from HB20-1, HB20-3, HB20-4
CC and HB20-25 in a carrier), a cell line producing the mAb, producing the
CC mAb, an antigen binding fragment of the mAb, an isolated nucleic acid
CC encoding a heavy chain or light chain comprising a variable region
CC (comprising CDR1, or CDR1 and CDR2 and CDR3 regions from mAb chosen from

CC HB20-1, HB20-3, HB20-4, HB20-5, HB20-25, MB20-11, MB20-1, MB20-2, MB20-7,
CC MB20-8, MB20-10, MB20-11, MB20-14, MB20-16 and MB20-18), a vector
CC comprising the nucleic acid, a cell comprising the nucleic acid or
CC vector, and depleting B cells in a mammalian subject (involving
CC administering the mAb and anti-CD22 or anti-CD19 antibody). The anti-CD20
CC mAb, compositions and cells are useful for depleting B cells in a
CC mammalian subject and for treating a B cell disorder. The B cell disorder
CC is B cell malignancy or autoimmune disease e.g. Rheumatoid arthritis,
CC idiopathic thrombocytopenic purpura or hemolytic anemia. The mammalian
CC subject is resistant to anti-CD20 mAb therapy or resistant to therapy
CC with mAb CD28. The mammalian subject has been or is currently treated
CC with chemotherapy. The mammalian subject had a relapse in a B cell
CC disorder. The mammalian subject is immunocompromised. The present
CC sequence represents a CDR (complementarity determining region) from anti-
CC CD20 monoclonal antibody.
XX
SQ Sequence 12 AA;

Query Match 41.7%; Score 30; DB 9; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 SVAKSVKSLYL 14
||:|:|:|
Db 1 SVSSSIRSNYL 11

RESULT 4
AEA46220
ID AEA46220 standard; peptide; 12 AA.
XX
AC AEA46220;
XX
DT 11-AUG-2005 (first entry)
XX
DE Apolipoprotein E C-terminal domain antibody VL-CDR1 peptide #118.
XX
KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotoxic;
KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
KW Alzheimer's disease; amyloidosis; Parkinson's disease; Huntingtons chorea;
KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW motor neurone disease; chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
PN GB2408508-A.
XX
PD 01-JUN-2005.
XX
PF 26-NOV-2004; 2004GB-00026043.
XX
PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR) ASTRAZENEGA AB.
XX
PA (DVAX-) DVAX CORP.
XX
PI Nordstedt C, Goldschmidt T, Henderlix M, Hoet R, Hoogenboom H;
XX Hufon S, Andersson CV, Lindquist J, Sunemark D, Leonov S;
XX
DR WPI: 2005-408785/42.
XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
XX e.g. Alzheimers disease.
XX
PS Example 23; Page 113; 392pp; English.
XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an

CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, Injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial atrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 12 AA;

Query Match 41.7%; Score 30; DB 9; Length 12;
Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 SVAKSVKSLYL 14
||:|:|:|
Db 1 SVGSVSSNLY 11

RESULT 5
ADM12121
ID ADM12121 standard; peptide; 9 AA.
XX
AC ADM12121;
XX
DT 07-APR-2005 (first entry)
XX
DE Human CD20 antigen peptide, SEQ ID No:219.
XX
KW Leukemic antigen; antigen; CD20; cytotoxic T-lymphocyte;
KW Immune stimulation; pharmaceutical; vaccine; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2005007673-A2.
XX
PD 27-JAN-2005.
XX
PF 02-JUL-2004; 2004WO-US021510.
XX
PR 03-JUL-2003; 2003US-0484689P.
XX
PA (UYRU-) UNIV RUSH MEDICAL CENT.
XX
PI Bae J;
XX
DR WPI: 2005-102081/11.
XX
PT New leukemic antigen comprising a fragment of CD19 or CD20 antigen, or
PT its variant or homolog, that is capable of stimulating a cytotoxic T-
PT lymphocyte reaction, useful for diagnosing, preventing or treating
XX diseases such as cancer.
XX
PS Example 1; SEQ ID NO 219; 69pp; English.
XX
CC The invention relates to isolated leukemic antigens comprising a fragment
CC of CD19 or CD20 antigen, or its mammalian homolog or variant that is
CC capable of stimulating a cytotoxic T-lymphocyte reaction. The fragment or
CC its variant is 8-80 amino acids in length, and the isolated leukemic
CC antigen is not a 44 amino acid extracellular domain of CD20. Also
CC described are (i) a method of stimulating an immune effector cell
CC response, (ii) an immune effector cell produced by the above method,
CC (iii) an antigen presenting cell produced by contacting the isolated
CC leukemic antigen cited above with an antigen presenting cell, (iv) an
CC isolated nucleic acid that encodes the above isolated leukemic antigen,
CC (v) a pharmaceutical composition comprising the isolated leukemic antigen

CC and a pharmaceutical carrier, and (v1) an antibody, or its functional
CC fragment, that is capable of binding the above isolated leukemic antigen.
CC The isolated leukemic antigen comprises any of SEQ ID NOS: 1-12 given in
CC the specification, or their variant having one or more conservative or
CC non-conservative amino acid substitutions. The leukemic antigens can be
CC included in a pharmaceutical composition such as a cancer vaccine. The
CC compositions and methods of the invention are useful for stimulating an
CC immune response against diseases such as cancer, or for diagnosing or
CC treating cancer. This sequence represents a CD20 antigen peptide tested
CC as a possible immunogenic epitope.

XX Sequence 9 AA;

Query Match 40.3%; Score 29; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 2,1e+06;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SVKSLVYG 15
|::|::|
Db 1 SIQSLFLG 8

RESULT 6
ADK40054
ID ADK40054 standard; peptide; 10 AA.

XX
AC ADK40054;

XX
DT 06-MAY-2004 (first entry)

XX
DE PNA molecule-related transporter peptide #226.

XX modified peptide nucleic acid; PNA; TP-L-PNA; TP; transporter peptide; L;
XX bond; linker; antibacterial; antimicrobial; cytostatic; virucide;
XX immunosuppressive; antisense-therapy; infectious disease;
XX bacterial infection; disinfection; cancer; bacterial; viral infection;
XX metabolic disease; immunological disorder.

XX Unidentified.

XX
XX WO2003092736-A2.

XX
XX 13-NOV-2003.

XX
XX 01-MAY-2003; 2003WO-DK000280.

XX
XX 01-MAY-2002; 2002DK-00000661.

XX
XX (PANT-) PANTHECO AS.

XX
XX Tolborg J, Frandsen TP, Nielsen BR, Johansen C, Kjaerulff S;

XX
XX WPI; 2004-011826/01.

XX
XX New modified peptide nucleic acid (PNA) molecule, useful in treating
XX and/or preventing cancer, viral infections, metabolic diseases,
XX immunological disorders, and in particular bacterial infections.

XX
XX Claim 6; Page 84; 96pp; English.

XX This invention relates to a novel modified peptide nucleic acid (PNA)
XX molecule. The invention comprises TP-L-PNA where TP transporter peptide;
XX L bond or a linker; PNA an oligomer of 4-35 monomers. The invention may
XX be useful for the development of compounds with an antibacterial,
XX anticancer, cytostatic, virucide or immunosuppressive. In addition,
XX the disclosed sequences could be used for antisense-therapy. The
XX compounds of the PNA molecule are useful in medicine, in particular for
XX the inactivation of the expression of specific genes by targeting the
XX genes at the mRNA, rRNA or DNA level. The PNA sequence is useful in the
XX treatment and/or prevention of infectious diseases, particularly
XX bacterial infections, or in disinfection of non-living objects. The
XX methods and compositions of the present invention are also useful for
XX treating cancer, bacterial and viral infections, metabolic diseases and

CC immunological disorders. The present sequence is that of a transporter
CC peptide which may be used during the creation of a PNA molecule of the
CC invention.

XX
XX Sequence 10 AA;

QY 3 FSVAKSVK 10
|::|::|
Db 3 FKVAKAVK 10

Query Match 40.3%; Score 29; DB 8; Length 10;
Best Local Similarity 75.0%; Pred. No. 2,8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
ADU08556
ID ADU08556 standard; peptide; 7 AA.

XX
AC ADU08556;

XX
DT 13-JAN-2005 (first entry)

XX
DE Heat shock protein binding peptide #85.

XX Hybrid antigen; antigenic domain; infectious agent; tumour antigen;
XX binding domain; heat shock protein; hsp; immune response;
XX infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.

XX Unidentified.

XX
XX WO2004091493-A2.

XX
XX 28-OCT-2004.

XX
XX 09-APR-2004; 2004WO-US010983.

XX
XX 11-APR-2003; 2003US-0462469P.

XX
XX 18-APR-2003; 2003US-0463746P.

XX
XX 16-SEP-2003; 2003US-0503417P.

XX
XX 12-FEB-2004; 2004US-00776521.

XX
XX 13-FEB-2004; 2004WO-US004340.

XX
XX 08-APR-2004; 2004US-00820067.

XX
XX (MOJA-) MOJAVE THERAPEUTICS INC.

XX
XX Flechtner JB, Prince-Cohane K, Mehta S, Slusaregicz P, Andjelic S,
XX Barber BH;

XX
XX WPI; 2004-775516/76.

XX
XX Hybrid antigen useful for treating an infectious disease or cancer,
XX comprises an antigenic domain from the infectious agent or cancer joined
XX to a heat shock protein binding domain through an improved linker
XX peptide.

XX
XX Disclosure; Page 32; 99pp; English.

XX The invention relates to hybrid antigens comprising at least one
XX antigenic domain of an infectious agent or tumour antigen, at least one
XX binding domain that non-covalently binds to a heat shock protein (hsp),
XX and at least one peptide linker between them. Also disclosed are: (a) a
XX composition for inducing an immune response to an infectious agent or
XX tumour antigen comprising at least one of the hybrid antigens or a
XX complex of at least one heat shock protein and at least one of the hybrid
XX antigens, (b) a method for inducing an immune response to an infectious
XX agent or tumour antigen by administering a hybrid antigen and a heat
XX shock protein, where the hybrid antigen and the heat shock protein are
XX non-covalently bound, and (c) treating an infectious disease or cancer by
XX administering a hybrid antigen and a heat shock protein. The heat shock
XX protein is preferably hsp70. The composition is administered via oral or
XX parenteral route. The hybrid antigen is useful in preparing a composition
XX for treating or preventing cancer or infectious disease. The new peptide

CC linkers give the antigens improved activity. Note: Many of the SEQ ID Nos
CC are replicated more than once in the specification but the sequences of
CC these replicated SEQ ID Nos are not the same. This sequence represents a
CC heat shock protein binding sequence.
XX

SQ Sequence 7 AA;

Query Match 38.9%; Score 28; DB 8; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYIG 15
|||:
Db 1 VKKLYIG 7

RESULT 8
ADU08445
ID ADU08445 standard; peptide; 8 AA.
XX
AC ADU08445;
XX
XX 18-NOV-2004 (first entry)
XX
DE Novel hybrid antigen-related peptide SegID315.

XX hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KW binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;
KW gene therapy; infectious disease; cancer.
XX unidentified.
XX
XX WO2004071457-A2.
XX
XX 26-AUG-2004.
XX
XX 13-FEB-2004; 2004WO-US004340.
XX
XX 13-FEB-2003; 2003US-0447142P.
XX
XX 11-APR-2003; 2003US-0462469P.
XX
XX 18-APR-2003; 2003US-0463746P.
XX
XX 16-SEP-2003; 2003US-0503417P.
XX
XX 12-FEB-2004; 2004US-00776521.
XX
XX (MOJA-) MOJAVE THERAPEUTICS INC.
XX
XX Pletcher J, Prince-Cohane K, Mehra S, Slusarewicz P, Andjelic S;
XX Barber B;
XX
XX WPI; 2004-625768/60.
XX
XX

PT New hybrid antigens comprising an antigenic domain and improved heat
PT shock protein-binding domains, useful for preventing or treating
PT infectious diseases or cancer.
XX

PS Disclosure; SEQ ID NO 315; 56pp; English.

CC This invention relates to a novel hybrid antigen which comprises at least
CC one antigenic domain of an infectious agent or tumour antigen and a
CC binding domain that non-covalently binds to a heat shock protein. The
CC invention may be useful for the production of compounds with an
CC antimicrobial or cytostatic activity. In addition, the invention may
CC prove useful for the production of a vaccine or for gene therapy. The
CC composition and methods disclosed are useful for preventing or treating
CC infectious diseases or cancer. The present sequence is that of a heat
CC shock protein binding domain peptide which was used in the
CC exemplification of the invention.
XX
XX

SQ Sequence 8 AA;

Query Match 38.9%; Score 28; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYIG 15
|||:
Db 1 VKKLYIG 7

RESULT 9
ADU08445
ID ADU08445 standard; peptide; 8 AA.
XX
AC ADU08445;
XX
XX 13-JAN-2005 (first entry)
XX
XX

DE Heat shock protein binding domain #195.

XX Hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KW binding domain; heat shock protein; hsp; immune response;
KW infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.
XX

XX Unidentified.
XX
XX
XX WO2004091493-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US010983.
XX
XX 11-APR-2003; 2003US-0462469P.
XX
XX 18-APR-2003; 2003US-0463746P.
XX
XX 16-SEP-2003; 2003US-0503417P.
XX
XX 12-FEB-2004; 2004US-00776521.
XX
XX 13-FEB-2004; 2004WO-US004340.
XX
XX 08-APR-2004; 2004US-00820067.
XX
XX (MOJA-) MOJAVE THERAPEUTICS INC.
XX
XX Pletcher J, Prince-Cohane K, Mehra S, Slusarewicz P, Andjelic S;
XX Barber B;
XX
XX WPI; 2004-775516/76.
XX
XX

PT Hybrid antigen useful for treating an infectious disease or cancer;
PT comprises an antigenic domain from the infectious agent or cancer joined
PT to a heat shock protein binding domain through an improved linker
PT peptide.
XX
XX

PS Disclosure; Page 42; 99pp; English.

CC The invention relates to hybrid antigens comprising at least one
CC antigenic domain of an infectious agent or tumour antigen, at least one
CC binding domain that non-covalently binds to a heat shock protein (hsp),
CC and at least one peptide linker between them. Also disclosed are: (a) a
CC composition for inducing an immune response to an infectious agent or
CC tumour antigen comprising at least one of the hybrid antigens or a
CC complex of at least one heat shock protein and at least one of the hybrid
CC antigens, (b) a method for inducing an immune response to an infectious
CC agent or tumour antigen by administering a hybrid antigen and a heat
CC shock protein, where the hybrid antigen and the heat shock protein are
CC non-covalently bound, and (c) treating an infectious disease or cancer by
CC administering a hybrid antigen and a heat shock protein. The heat shock
CC protein is preferably hsp70. The composition is administered via oral or
CC parenteral route. The hybrid antigen is useful in preparing a composition
CC for treating or preventing cancer or infectious disease. The new peptide
CC linkers give the antigens improved activity. Note: Many of the SEQ ID Nos
CC are replicated more than once in the specification but the sequences of
CC these replicated SEQ ID Nos are not the same. This sequence represents a
CC heat shock protein binding sequence.
XX
XX

SQ Sequence 8 AA;

Query Match 38.9%; Score 28; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 9 VKSLYLIG 15
Db 1 VKKLYIG 7

RESULT 10
ADU08841
ID ADU08841 standard; peptide; 8 AA.

AC ADU08841;

DT 13-JAN-2005 (first entry)

DE Heat shock protein binding domain #491.

KM Hybrid antigen; antigenic domain; infectious agent; tumour antigen;

KW binding domain; heat shock protein; hsp; immune response;

OS Infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.

XX Unidentified.

XX MO2004091493-A2.

XX 28-OCT-2004.

XX 09-APR-2004; 2004MO-US010983.

XX 11-APR-2003; 2003US-0462469P.

XX 18-APR-2003; 2003US-0463746P.

XX 16-SEP-2003; 2003US-0503417P.

XX 12-FEB-2004; 2004US-00776521.

XX 13-FEB-2004; 2004MO-US004340.

XX 08-APR-2004; 2004US-00820067.

XX (MOJA-) MOJAVE THERAPEUTICS INC.

XX Flechtner JB, Prince-Cohane K, Mehta S, Slusaregicz P, Andjelic S;

XX Barber BH;

XX WPI; 2004-775516/76.

XX Hybrid antigen useful for treating an infectious disease or cancer,

XX PT comprises an antigenic domain from the infectious agent or cancer joined

XX PT to a heat shock protein binding domain through an improved linker

XX peptide.

XX Disclosure; Page 44; 99pp; English.

XX The invention relates to hybrid antigens comprising at least one

XX antigenic domain of an infectious agent or tumour antigen, at least one

XX binding domain that non-covalently binds to a heat shock protein (hsp),

XX and at least one peptide linker between them. Also disclosed are: (a) a

XX composition for inducing an immune response to an infectious agent or

XX tumour antigen comprising at least one of the hybrid antigens or a

XX complex of at least one heat shock protein and at least one of the hybrid

XX antigens, (b) a method for inducing an immune response to an infectious

XX agent or tumour antigen by administering a hybrid antigen and a heat

XX shock protein, where the hybrid antigen and the heat shock protein are

XX non-covalently bound, and (c) treating an infectious disease or cancer by

XX administering a hybrid antigen and a heat shock protein. The heat shock

XX protein is preferably hsp70. The composition is administered via oral or

XX parenteral route. The hybrid antigen is useful in preparing a composition

XX for treating or preventing cancer or infectious disease. The new peptide

XX linkers give the antigens improved activity. Note: Many of the SEQ ID Nos

XX are replicated more than once in the specification but the sequences of

XX these replicated SEQ ID Nos are not the same. This sequence represents a

XX heat shock protein binding sequence.

XX Sequence 8 AA;

XX Query Match 38.9%; Score 28; DB 8; Length 8;

Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLIG 15
Db 1 VKKLYIG 7

RESULT 11
ADT73328
ID ADT73328 standard; peptide; 9 AA.

AC ADT73328;

DT 13-JAN-2005 (first entry)

DE Human RSV N high affinity binding peptide SegID 1224.

XX human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;

XX MHC epitope; DNA-based immunisation; RSV infection; viral; vaccine.

XX Human respiratory syncytial virus.

XX MO2004092207-A2.

XX 28-OCT-2004.

XX 16-APR-2004; 2004MO-EP004061.

XX 16-APR-2003; 2003EP-00447095.

XX (ALGO-) ALGONOMICS NV.

XX Lasters I, Desmet J, Stegmann T;

XX WPI; 2004-758334/74.

XX New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N

XX PT or P) for inducing an immune response to RSV or for diagnosing,

XX PT preventing or treating viral infections, particularly RSV infection.

XX Disclosure; SEQ ID NO 1224; 143pp; English.

XX This invention relates to novel isolated or purified peptides of the

XX human respiratory syncytial virus (RSV), in particular ten RSV genes

XX encoding 11 separate viral proteins: non-structural proteins NS-1 (also

XX known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and

XX eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and

XX SH (also known as the 1A protein). Specifically, it refers to a

XX composition comprising an above peptide mixed with a pharmaceutical

XX excipient or an RSV immunogenic composition comprising a recombinant

XX expression vector with a nucleic acid insert encoding an above peptide.

XX The present invention describes an in vitro method of detecting cytotoxic

XX T lymphocytes (CTLs) that respond to a major histocompatibility complex

XX (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The

XX RSV peptide is useful for preparing a diagnostic composition or an RSV

XX (prophylactic or therapeutic) vaccine composition for a DNA-based

XX immunisation, or for preparing an immune response provoking vaccine in

XX the event of RSV infection (the vaccine being prepared by contacting the

XX polypeptide in an immune response-provoking amount of specific CTL).

XX Accordingly, these peptide compositions have viral activity. This

XX peptide sequence is a human RSV high binding affinity peptide of the

XX invention.

XX Sequence 9 AA;

XX Query Match 38.9%; Score 28; DB 8; Length 9;

XX Best Local Similarity 66.7%; Pred. No. 2.1e+06;

XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX QY 6 AKSVKSLYL 14

XX Db 1 AKSVKNIML 9

```
RESULT 12
AAE00650
ID AAE00650 standard; protein; 11 AA.
XX
XX
AC AAE00650;
XX
XX 02-JUL-2001 (first entry)
XX
XX Alpha-1,2 mannosidase protein #2.
XX
XX Alpha-1,2 mannosidase; glycosylation pattern; glycoprotein.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 2 /label= Unknown
XX FT
XX FT WO200125406-A1.
XX
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027210.
XX
XX 01-OCT-1999; 99US-0157341P.
XX
XX (UUYI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
XX Hintz WE, Eades CJ;
XX
XX WPI; 2001-290610/30.
XX
XX New mannosidase enzymes, useful for modifying or altering the
XX glycosylation patterns of macromolecules, particularly for modifying
XX target protein.
XX
XX Example 9; Page 40; 87pp; English.
XX
XX The invention relates to Aspergillus nidulans alpha-1,2 mannosidase genes
XX and proteins. The mannosidase enzymes are useful for modifying or
XX altering the glycosylation patterns of macromolecules, e.g. protein. In
XX particular, the enzymes useful for modifying target proteins. This
XX enables glycoproteins to be engineered to be more effectively used and
XX produced. The present sequence is alpha-1,2 mannosidase protein. The
XX MARRENV3B forward primer is designed from the complement of the reverse
XX translation of this sequence. Note: This sequence is stated as being the
XX same as that shown as SEQ ID NO:14 in the sequence listing of the
XX specification. However this sequence has additional 2 residues at its N-
XX terminal end
XX
XX Sequence 11 AA;
XX
XX Query Match 38.9%; Score 28; DB 4; Length 11;
XX Best Local Similarity 45.5%; Pred. No. 4.7e+02;
XX Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 FSVAKSVKSLY 13
XX |::|::|
XX Db 1 FXLAETLKYLY 11
XX
XX RESULT 13
XX ID AAB97744 standard; peptide; 15 AA.
XX
XX AC AAB97744;
XX
XX 06-AUG-2003 (revised)
XX DT 08-AUG-2001 (first entry)
XX
XX gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:37.
```

```
XX
XX Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;
XX tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;
XX cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.
XX
XX OS Viruses.
XX OS Synthetic.
XX
XX PN WO200130382-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-CA001253.
XX
XX 22-OCT-1999; 99US-0160879P.
XX PR 07-AUG-2000; 2000US-0223325P.
XX
XX (AVET ) AVENTIS PASTEUR LTD.
XX
XX Bernstein N, Tartaglia J, Moingeon P, Barber B;
XX
XX WPI; 2001-308587/32.
XX
XX Inducing immune response to tumor antigen, useful in immunotherapy of
XX cancer, by administering the antigen to a lymphatic site.
XX
XX Example 1; Page 39; 60pp; English.
XX
XX The present invention describes a method for inducing an immune response,
XX in an animal, to a tumour antigen (Ag) comprising administering Ag, or
XX nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys
XX (Macaca fascicularis) were injected with a modified form of gp100 antigen
XX (a) into the left inguinal lymph node or (b) subcutaneously. Both animals
XX of (a) developed a cell-mediated response (indicated by production of
XX interferon-gamma from T lymphocytes when exposed to gp100 peptides), but
XX only 2 of 4 animals of (b) did so. Also animals in (a) produced a far
XX greater antibody response to gp100. The method is used in immunotherapy
XX of a wide range of cancers through induction of a specific immune
XX response (humoral and cellular) against the tumour antigens. When
XX administered to a lymphatic site, Ag (or (I)) induces a stronger immune
XX response than administration by other routes and may also break tolerance
XX to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to
XX AAB97815 represent peptides derived from gp100 which stimulate interferon
XX (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given
XX in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)
XX protein given in AAB97817; and AAB97818 represents a CEA modified antigen
XX peptide, all of which are used in the exemplification of the present
XX invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 15 AA;
XX
XX Query Match 38.9%; Score 28; DB 4; Length 15;
XX Best Local Similarity 75.0%; Pred. No. 6.7e+02;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 VPFVSVAKS 8
XX |||||
XX Db 8 VPFVSVSVS 15
XX
XX RESULT 14
XX ID AAB97745 standard; peptide; 15 AA.
XX
XX AC AAB97745;
XX
XX 06-AUG-2003 (revised)
XX DT 08-AUG-2001 (first entry)
XX
XX gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:38.
XX
XX Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;
XX tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;
```

KM cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.
 XX
 XX Varises.
 OS Synthetic.
 XX
 PN WO200130382-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-CA001253.
 XX
 PR 22-OCT-1999; 99US-0160879P.
 PR 07-AUG-2000; 2000US-0223325P.
 XX
 PA (AVERT) AVENTIS PASTEUR LTD.
 XX
 PI Berinstein N, Tartaglia J, Moingeon P, Barber B;
 DR WPI; 2001-308587/32.
 XX
 PT Inducing immune response to tumor antigen, useful in immunotherapy of
 cancer, by administering the antigen to a lymphatic site.
 XX
 PS Example 1; Page 39; 60pp; English.
 XX
 CC The present invention describes a method for inducing an immune response,
 CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or
 CC nucleic acid (1) that encodes it, to a lymphatic site. Cynomolgus monkeys
 CC (Macaca fascicularis) were injected with a modified form of gp100 antigen
 CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals
 CC of (a) developed a cell-mediated response (indicated by production of
 CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but
 CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far
 CC greater antibody response to gp100. The method is used in immunotherapy
 CC of a wide range of cancers through induction of a specific immune
 CC response (humoral and cellular) against the tumour antigens. When
 CC administered to a lymphatic site, Ag (or (1)) induces a stronger immune
 CC response than administration by other routes and may also break tolerance
 CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to
 CC AAB97815 represent peptides derived from gp100 which stimulate interferon
 CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given
 CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)
 CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen
 CC peptide, all of which are used in the exemplification of the present
 CC invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 38.9%; Score 28; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPPSVAKS 8
 |||||:
 DB 3 VPPSVSVS 10
 RESULT 15
 AAB98135
 ID AAB98135 standard; peptide; 15 AA.
 XX
 AC AAB98135;
 XX
 DT 17-AUG-2001 (first entry)
 XX
 DE Interferon-gamma stimulation gp100 derived peptide 1369.
 XX
 KM Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
 KM modified gp100; vaccine; gene therapy; cancer.
 OS Homo sapiens.
 XX
 PN WO200130847-A1.

XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-CA001254.
 XX
 PR 22-OCT-1999; 99US-0160879P.
 PR 07-AUG-2000; 2000US-0223325P.
 XX
 PA (AVERT) AVENTIS PASTEUR LTD.
 XX
 PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
 DR WPI; 2001-316326/33.
 XX
 PT New isolated and purified gp100 useful for the prophylactic treatment of
 cancer.
 XX
 PS Example 4; Page 61; 89pp; English.
 XX
 CC The present invention describes an isolated and purified modified gp100
 CC molecule (gp100M) capable of modulating an immune response in an animal.
 CC gp100M has cytostatic activity and can be used in vaccine production and
 CC gene therapy. Nucleic acids and proteins of the invention are useful as
 CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
 CC AAB98098 to AAB98206 represent sequence used in the exemplification of
 CC the present invention. More specifically AAB98098 to AAB98205 represent
 CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
 CC AAH22106 represent primers used in the present invention; AAH22099
 CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
 CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
 CC gp100M protein given in AAB22106
 XX
 SQ Sequence 15 AA;
 Query Match 38.9%; Score 28; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPPSVAKS 8
 |||||:
 DB 3 VPPSVSVS 10
 RESULT 16
 AAB98134
 ID AAB98134 standard; peptide; 15 AA.
 XX
 AC AAB98134;
 XX
 DT 17-AUG-2001 (first entry)
 XX
 DE Interferon-gamma stimulation gp100 derived peptide 1368.
 XX
 KM Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
 KM modified gp100; vaccine; gene therapy; cancer.
 OS Homo sapiens.
 XX
 PN WO200130847-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-CA001254.
 XX
 PR 22-OCT-1999; 99US-0160879P.
 PR 07-AUG-2000; 2000US-0223325P.
 XX
 PA (AVERT) AVENTIS PASTEUR LTD.
 XX
 PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
 DR WPI; 2001-316326/33.
 XX

PT New isolated and purified gp100 useful for the prophylactic treatment of
PT cancer.
XX
PS Example 4; Page 61; 89pp; English.
XX
CC The present invention describes an isolated and purified modified gp100
CC molecule (gp100M) capable of modulating an immune response in an animal.
CC gp100M has cytostatic activity and can be used in vaccine production and
CC gene therapy. Nucleic acids and proteins of the invention are useful as
CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
CC AAB98098 to AAB98206 represent sequence used in the exemplification of
CC the present invention. More specifically AAB98098 to AAB98205 represent
CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
CC AAH22106 represent primers used in the present invention; AAH22099
CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
CC gp100M protein given in AAB22106
XX
SQ Sequence 15 AA;
Query Match 38.9%; Score 28; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPPSVAKS 8
DB 8 VPPSVSVS 15
RESULT 17
ABP73086
ID ABP73086 standard; peptide; 15 AA.
XX
XX ABP73086;
AC
XX
DT 17-JUN-2003 (first entry)
XX
XX Amino acid sequence of an epitope derived from KSHV.
DE
XX
XX Epitope; KSHV; CD8 T cell; vaccine; dendritic cell; T lymphocyte.
KM
XX
OS Synthetic.
OS Kaposi's sarcoma herpesvirus.
XX
XX WO2003014154-A2.
XX
XX 20-FEB-2003.
PD
XX
PF 05-AUG-2002; 2002WO-GB003594.
XX
XX 03-AUG-2001; 2001GB-00019038.
PR
XX
XX (UNLO) UNIV COLLEGE LONDON.
PA
XX
PI Boshoff C;
XX
XX WPI; 2003-289909/28.
DR
XX
PT New polypeptides and expression vectors with an epitope sequence
PT recognized by a CD8 T cell, useful in the manufacture of a vaccine for
PT the prophylactic and/or therapeutic treatment of Kaposi's sarcoma
PT herpesvirus infection.
PT
XX
PS Claim 2; Page 49; 58pp; English.
XX
CC The present sequence represents an epitope, of a formula given in the
CC specification. The epitope is derived from Kaposi's sarcoma herpesvirus
CC (KSHV), and is recognised by CD8 T cells. Polypeptides comprising the
CC epitope are useful for producing a vaccine against KSHV. They are also
CC useful for stimulating dendritic cells or T lymphocytes ex vivo
XX
SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 6.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 8 SVKSLYLK 15
DB 8 SLSSTLYG 15
RESULT 18
ABR30675
ID ABR30675 standard; peptide; 15 AA.
XX
XX ABR30675;
AC
XX
DT 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 83P4B8 HLA peptide #1737.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KM
XX
XX human leukocyte antigen.
KM
XX
OS Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US011654.
PP
XX
XX 10-APR-2001; 2001US-0282739P.
PR
XX
XX 10-APR-2001; 2001US-0283112P.
PR
XX
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI
XX
XX Morrison K, Morrison RK, Raltano AB;
PI
XX
DR WPI; 2003-075555/07.
XX
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 479; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX
SQ Sequence 15 AA;
Query Match 38.9%; Score 28; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 14
DB 2 SVKSFRLQL 12
RESULT 19

ABR31599
 ID ABR31599 standard; peptide; 15 AA.
 XX
 AC ABR31599;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #2661.
 XX
 KM Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 XX 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 495; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 SQ Sequence 15 AA;
 XX
 QY
 DB 4 SVAKSVKSLYL 14
 3 SVVKSFRDQL 13
 XX
 QY 4 SVAKSVKSLYL 14
 DB 3 SVVKSFRDQL 13
 XX
 RESULT 20
 ID ABR31127 standard; peptide; 15 AA.
 XX
 AC ABR31127;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #2189.
 XX
 KM Human; cytostatic; vaccine; cancer; immune response; HLA;

KM human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 XX 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 487; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 SQ Sequence 15 AA;
 XX
 QY
 DB 4 SVAKSVKSLYL 14
 2 SVVKSFRDQL 12
 XX
 QY 4 SVAKSVKSLYL 14
 DB 2 SVVKSFRDQL 12
 XX
 RESULT 21
 ID ABR30768 standard; peptide; 15 AA.
 XX
 AC ABR30768;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #1830.
 XX
 KM Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PR 10-APR-2002; 2002WO-US011654.
 XX

PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 481; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
SQ Sequence 15 AA;
XX
Query Match 38.9%; Score 28; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 14
DB 2 SVKSFKDQL 12
XX
RESULT 22
ABR31373
ID ABR31373 standard; peptide; 15 AA.
XX
AC ABR31373;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 83P4B8 HLA peptide #2435.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.

XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 491; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
SQ Sequence 15 AA;
XX
Query Match 38.9%; Score 28; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 14
DB 3 SVKSFKDQL 13
XX
RESULT 23
ABR30871
ID ABR30871 standard; peptide; 15 AA.
XX
AC ABR30871;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 83P4B8 HLA peptide #1933.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 482; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the of
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 8; Length 15;
 Best Local Similarity 63.6%; Pred. No. 6.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 SVAKSVKSLYL 14
 Db 3 SVVKSFKDLQL 13

RESULT 24

ID ADN71829 standard; peptide; 15 AA.

XX ADN71829;

DT 01-JUL-2004 (first entry)

XX Human 273P4B7v.1 protein epitope #5792.

XX 273P4B7; human; cancer; tumour; epitope.

XX Homo sapiens.

XX PN WO2004016762-A2.

XX PD 26-FEB-2004.

XX PF 15-AUG-2003; 2003WO-US025665.

XX PR 16-AUG-2002; 2002US-0404306P.

XX PR 01-NOV-2002; 2002US-0423290P.

XX PA (AGEN-) AGENSYS INC.

XX PI Chailita-Eid PM, Faris M, Raitano AB, Jakobovits A, Ge W;

XX DR WPI; 2004-203790/19.

XX PT New composition comprising 273P4B7 proteins, useful for detecting and

XX PS treating cancer by inhibiting the growth or viability of cancer cells.

XX PS Claim 1; Fig 2A; 268bp; English.

CC The invention relates to a composition comprising 273P4B7 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VII-IX.

XX SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 8; Length 15;
 Best Local Similarity 54.5%; Pred. No. 6.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPPSVAKSVKS 11
 Db 3 IPSSVKNKSMNS 13

RESULT 25

ID ADN71169 standard; peptide; 15 AA.

XX ADN71169;

DT 01-JUL-2004 (first entry)

XX Human 273P4B7v.1 protein epitope #5132.

XX 273P4B7; human; cancer; tumour; epitope.

XX Homo sapiens.

XX PN WO2004016762-A2.

XX PD 26-FEB-2004.

XX PF 15-AUG-2003; 2003WO-US025665.

XX PR 16-AUG-2002; 2002US-0404306P.

XX PR 01-NOV-2002; 2002US-0423290P.

XX PA (AGEN-) AGENSYS INC.

XX PI Chailita-Eid PM, Faris M, Raitano AB, Jakobovits A, Ge W;

XX DR WPI; 2004-203790/19.

XX PT New composition comprising 273P4B7 proteins, useful for detecting and

XX PS treating cancer by inhibiting the growth or viability of cancer cells.

XX PS Claim 1; Fig 2A; 268bp; English.

CC The invention relates to a composition comprising 273P4B7 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VII-IX.

XX SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 8; Length 15;
 Best Local Similarity 54.5%; Pred. No. 6.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPPSVAKSVKS 11
 Db 4 IPSSVKNKSMNS 14

RESULT 26

ID ADN71392 standard; peptide; 15 AA.

XX ADN71392;

DT 01-JUL-2004 (first entry)

XX Human 273P4B7v.1 protein epitope #5355.

XX 273P4B7; human; cancer; tumour; epitope.

XX Homo sapiens.

XX PN WO2004016762-A2.

XX PD 26-FEB-2004.

XX PF 15-AUG-2003; 2003WO-US025665.

XX PR 16-AUG-2002; 2002US-0404306P.

XX PR 01-NOV-2002; 2002US-0423290P.

```
XX (AGEN-) AGENSYS INC.
XX Chailita-Eid PM, Faris M, Raitano AB, Jakobovits A, Ge W;
XX WPI: 2004-203790/19.
XX
XX New composition comprising 273P4B7 proteins, useful for detecting and
XX treating cancer by inhibiting the growth or viability of cancer cells.
XX Claim 1; Fig 2A; 268bp; English.
XX
XX The invention relates to a composition comprising 273P4B7 proteins. The
XX composition and proteins are useful for detecting and treating cancer by
XX inhibiting the growth or viability of cancer cells. The present sequence
XX represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
XX Note the epitope sequences are displayed in tables VIII-XLIX.
XX
XX Sequence 15 AA;
SQ
Query Match          38.9%; Score 28; DB 8; Length 15;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSAVAKSVKS 11
Db 4 IPFSVAKSMNS 14
RESULT 27
ADN70835
ID ADN70835 standard; peptide; 15 AA.
AC ADN70835;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human 273P4B7v.1 protein epitope #4798.
XX
XX 273P4B7; human; cancer; tumour; epitope.
XX
XX Homo sapiens.
XX
XX WO2004016762-A2.
XX
XX 26-FEB-2004.
XX
XX 15-AUG-2003; 2003WO-US025665.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Chailita-Eid PM, Faris M, Raitano AB, Jakobovits A, Ge W;
XX
XX WPI: 2004-203790/19.
XX
XX New composition comprising 273P4B7 proteins, useful for detecting and
XX treating cancer by inhibiting the growth or viability of cancer cells.
XX Claim 1; Fig 2A; 268bp; English.
XX
XX The invention relates to a composition comprising 273P4B7 proteins. The
XX composition and proteins are useful for detecting and treating cancer by
XX inhibiting the growth or viability of cancer cells. The present sequence
XX represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
XX Note the epitope sequences are displayed in tables VIII-XLIX.
XX
XX Sequence 15 AA;
SQ
Query Match          38.9%; Score 28; DB 8; Length 15;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
```

```
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSAVAKSVKS 11
Db 4 IPFSVAKSMNS 14
RESULT 28
AA59641
ID AA59641 standard; peptide; 14 AA.
XX
XX AA59641;
XX
XX 27-MAR-2000 (first entry)
XX
XX HIV replication inhibitor peptide #2.
XX
XX Human immunodeficiency virus; HIV replication inhibitor; HIV infection;
XX viral replication.
XX
XX Homo sapiens.
XX
XX WO957272-A1.
XX
XX 11-NOV-1999.
XX
XX 03-MAY-1999; 99WO-US009654.
XX
XX 04-MAY-1998; 98US-0084076P.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Klotman ME, Mosolan A, Tel Xeira A;
XX
XX WPI: 2000-086412/07.
XX
XX Novel HIV replication inhibitor peptides for treating individuals
XX infected with or exposed to HIV.
XX
XX Claim 2; Page 7; 48pp; English.
XX
XX This is a human immunodeficiency virus (HIV) replication inhibitor
XX peptide. The peptide has the following properties: (a) isolated from CD8+
XX cells (especially cell line K1 50K); (b) inhibits the replication of HIV
XX Ba-1 in macrophages and HIV IIIB in CD4+ cells; (c) is not a cytokine
XX selected from RANTES (regulated on activation normal T-cell expressed and
XX secreted), MIP-1alpha or MIP-1b (macrophage inhibitory protein); (d) a
XX molecular weight of approximately 8 kDa; (e) inhibits the replication of
XX HIV in the viral life cycle following reverse transcription but before
XX integration into the cellular genome; (f) is stable at pH 2; (g)
XX maintains activity after being subjected to freezing and thawing; and (h)
XX CC optionally comprises this amino acid sequence or alternatively AA59640.
XX The polypeptides are used to inhibit HIV viral replication in individuals
XX infected with or exposed to HIV
XX
XX Sequence 14 AA;
SQ
Query Match          38.2%; Score 27.5; DB 3; Length 14;
Best Local Similarity 69.2%; Pred. No. 7.7e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 VPFSAVAKSVKSLY 13
Db 3 VEASVA-SVRSLY 14
RESULT 29
AAU97491
ID AAU97491 standard; peptide; 14 AA.
XX
XX AAU97491;
XX
XX 29-AUG-2003 (revised)
```


DT 13-AUG-2002 (first entry)
XX Human immunodeficiency virus (HIV) replication inhibitor peptide #2.
DE
XX
XX Human immunodeficiency virus; replication inhibitor; CD8+ cells;
KW acquired immunodeficiency syndrome; AIDS; AIDS-related complex;
XX asymptomatic; anti-HIV; HIV inhibitor.
OS Human immunodeficiency virus 1.
XX
XX US6358511-B1.
PN
XX 19-MAR-2002.
PD
XX 03-MAY-1999; 99US-00305781.
PF
XX 03-MAY-1999; 99US-00305781.
PR
XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
PA
XX Klotman ME, Arevik M, Avelino T;
PI
XX WPI; 2002-433310/46.
DR
XX
XX New inhibitors of HIV replication comprise a peptide or polypeptide with
PT a defined amino acid sequence, and are derived from e.g., CD8+ cells.
PS
XX Claim 2; Col 15; 21pp; English.
SQ
XX The present invention relates to new inhibitors of HIV replication
CC comprising a peptide or polypeptide with a defined amino acid sequence
CC and are derived from e.g. CD8+ cells. The inhibitors are useful in
CC treating HIV-positive individuals, including those with AIDS (acquired
CC immunodeficiency syndrome) and AIDS-related complex as well as
CC asymptomatic individuals. The present amino acid sequence represents
CC human immunodeficiency virus (HIV) replication inhibitor peptide #2 of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 14 AA:
XX
XX Query Match 38.2%; Score 27.5; DB 5; Length 14;
XX Best Local Similarity 69.2%; Pred. No. 7.7e+02;
XX Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 VPSPVAKSVKSLY 13
DB 3 VESVA-SVRSLY 14
XX
RESULT 30
ADI44462
ID ADI44462 standard; peptide; 11 AA.
XX
AC ADI44462;
XX
DT 22-APR-2004 (first entry)
XX
DE C. dactylon basic group 4 allergen fragment #1.
XX
XX Immunomodulatory; T cell-reactive; Group 4; Poaceae; major allergen;
KW hypallergenic; antiallergic; vaccine; hyposensitisation;
KW desensitisation; immunoglobulin E.
XX
OS Cynodon dactylon.
XX
XX WO2004000881-A1.
PN
XX 31-DEC-2003.
PD
XX 11-JUN-2003; 2003WO-EP006092.
PF
XX 25-JUN-2002; 2002EP-00013953.
PR
XX

PA (MERE) MERCK PATENT GMBH.
XX
XX Fiebig H, Nandy A, Suck R, Cromwell O, Petersen A, Becker W;
PI
XX WPI; 2004-071723/07.
DR
XX
XX New nucleic acid encoding the Phl p4 major allergen of Phleum pratense,
PT useful for DNA vaccination, also derived proteins, useful for
PT hyposensitization and diagnosis.
PS
XX Disclosure; SEQ ID NO 14; 73pp; German.
XX
XX This invention describes a novel polynucleotide which has the properties
CC of the immunomodulatory, T cell-reactive form of a Group 4 Poaceae major
CC allergen, Phl p 4 and can be altered by targeted mutation of an
CC individual codon, elimination or addition to form hypoallergenic mutants.
CC The products of the invention are antiallergic and can be used in
CC vaccines or for hyposensitisation. The polynucleotide, also related
CC sequences encoding Poaceae allergens, derived expression vectors and the
CC encoded polypeptides, are useful for treatment and/or prevention of
CC allergy caused by Group 4 Poaceae allergens, especially by
CC immunotherapeutic DNA vaccination or desensitisation in humans or other
CC animals. The polypeptides can also be used for diagnosis of such
CC allergies, in vivo or in vitro, by detecting specific immunoglobulin E.
CC This sequence represents a basic group 4 allergen peptide fragment from
CC Cynodon dactylon described in the disclosure of the invention.
XX
SQ Sequence 11 AA:
XX
XX Query Match 37.5%; Score 27; DB 8; Length 11;
XX Best Local Similarity 62.5%; Pred. No. 7.2e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 7 KSVKSLYL 14
DB 1 KTVKPLYI 8
XX
RESULT 31
AEB28067
ID AEB28067 standard; peptide; 11 AA.
XX
AC AEB28067;
XX
DT 08-SEP-2005 (first entry)
XX
DE Cynodon dactylon Group 4 allergenic peptide SEQ ID 17.
XX
XX allergen; pollen; cereal; Sec c 4; Hor v 4; Tri a 4; vaccine; allergy;
KW antiallergic; immune disorder; diagnosis; plant.
XX
OS Cynodon dactylon.
XX
XX WO2005059136-A2.
PN
XX 30-JUN-2005.
PD
XX 01-DEC-2004; 2004WO-EP013664.
PF
XX 16-DEC-2003; 2003DE-01059351.
PR
XX (MERE) MERCK PATENT GMBH.
PA
XX Fiebig H, Nandy A, Cromwell O;
PI
XX WPI; 2005-521939/53.
DR
XX
XX New DNA encoding major allergens from rye, barley and wheat pollen, and
PT derived polypeptides, useful for treatment and diagnosis of allergy.
XX
PS Disclosure; SEQ ID NO 17; 61pp; German.
XX
XX This invention describes novel DNA molecules, corresponding to the
CC

CC sequence of the major allergens of cereal pollen. The invention also
CC describes; 1) DNA that hybridizes to the novel cereal allergens under
CC stringent conditions and is derived from Poaceae; 2) DNA that encodes a
CC polypeptide that is immunologically cross-reactive with the major
CC allergens Sec c 4 from Secale cereale, Hor v 4 from Hordeum vulgare or
CC Tri a 4 from Triticum aestivum and derived from Poaceae; 3) a DNA
CC fragment, or combination of fragments, that encode an immunomodulatory T-
CC cell reactive fragment of Group 4 Poaceae allergens; 4) a DNA
CC corresponding to any of the new DNAs or fragments that encodes an
CC immunomodulatory T-cell reactive fragment but is modified by targeted
CC mutation of individual codons, deletion or addition; 5) a recombinant DNA
CC expression vector or cloning system containing any of the new DNAs linked
CC to expression control sequences; 6) a host organism transformed with any
CC of the new DNAs or the vector of 5) and 7) preparing a polypeptide
CC encoded by the new DNAs by culturing the organisms of 6). Primers were
CC designed from the known DNA sequence for the Phl p 4 (Phleum pratense)
CC allergen and tested for amplification of DNA from rye pollen. The partial
CC sequences obtained were used to screen expressed sequence tag (EST) data
CC bases; the partial sequences aligned and new primers designed for
CC amplification of further sequence fragments, allowing construction of the
CC sequences (two isoforms) for Sec c 4. The Sec c 4 sequences obtained were
CC used to screen EST data bases from wheat and barley to identify the other
CC novel polypeptides. The novel polynucleotides and vectors containing
CC them, are used for immunotherapeutic vaccination against allergies
CC induced by Group 4 Poaceae allergens. Polypeptides can be used similarly,
CC also for diagnosis (in vivo or in vitro) of such allergies or in a
CC vaccine. This sequence represents a group 4 allergenic peptide from
CC Cynodon dactylon (bermuda grass).

CC Sequence 11 AA;

Query Match 37.5%; Score 27; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 KSVKSLYL 14
||:|:|:|:
Db 1 KTVKPLYL 8

RESULT 32
AEB13465
ID AEB13465 standard; peptide; 11 AA.

AC AEB13465;

DT 08-SEP-2005 (first entry)

DE Cynodon dactylon group 4 allergen fragment SEQ ID NO 11.

KW grass pollen; allergen; lol p 4; pollen; diagnosis; vaccine;
KM group 4 allergen.

OS Cynodon dactylon.

PN WO2005058936-A2.

PD 30-JUN-2005.

PF 01-DEC-2004; 2004MO-BP013663.

PR 16-DEC-2003; 2003DE-01059352.

PA (MERE) MERCK PATENT GMBH.

PI Fiebig H, Nandy A, Cromwell O;

DR WPI; 2005-506110/51.

For the treatment/prevention of the main grass pollen allergies, a DNA
PT molecule is selected for hybridizing to give a wide variety of agents
PT with a hypoallergenic effect.

PS Disclosure; SEQ ID NO 11; 38pp; German.

XX This invention describes a novel method for the preparation of a DNA
CC molecule encoding the main grass pollen allergen lol p 4. The invention
CC also describes fragments, new combinations of partial sequences and point
CC mutants which have a hypoallergenic effect. The recombinant DNA molecules
CC and the derived polypeptides, fragments, combinations of partial
CC sequences and variants are for the treatment of pollen allergies. They
CC can also be used for in vitro and in vivo diagnosis of pollen allergies.
CC The products of the invention can be used as a pharmaceutical for
CC immunotherapeutic vaccination against lol p 4 allergies and/or for the
CC prevention of such allergies. This sequence represents a fragment of the
CC Cynodon dactylon group 4 allergen.

CC Sequence 11 AA;

Query Match 37.5%; Score 27; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 KSVKSLYL 14
||:|:|:|:
Db 1 KTVKPLYL 8

RESULT 33
ADM47132
ID ADM47132 standard; peptide; 12 AA.

AC ADM47132;

DT 24-MAR-2005 (first entry)

DE Anti-CD20 monoclonal antibody light chain MHB20-8.10 CDR 1.

KW CD20; monoclonal antibody; rheumatoid arthritis; antiarthritis;
KM antirheumatic; immune disorder; inflammation; musculoskeletal disease;
KW idiopathic thrombocytopenic purpura; hemostatic; hemolytic anemia.

OS Mus musculus.

PN WO2005000901-A2.

PD 06-JAN-2005.

PF 07-MAY-2004; 2004MO-US014326.

PR 09-MAY-2003; 2003US-0469451P.

PA (UYDU-) UNIV DUKE.

PI Tedder TF, Uchida J, Hamaguchi Y, Poe JC;

DR WPI; 2005-066556/07.

Novel monoclonal antibody (mab) binding to CD20 or mouse CD20, in which
PT density of binding of mab to B cells is two-fold higher than density of
PT binding of mab1F5 to B cells, useful for depleting B cells, and treating
XX B cell disorder.

Example 1; SEQ ID NO 91; 205pp; English.

XX The invention relates to a monoclonal antibody (mab) or its antigen-
CC binding fragment that specifically binds to human CD20 or mouse CD20,
CC where the density of binding of mab or antigen-binding fragment of mab 1F5
CC cells is at least two-fold higher than the density of binding of mab 1F5
CC to B cells. Also included are a pharmaceutical composition comprising mab
CC in a carrier, a pharmaceutical composition (comprising mab or its antigen
CC binding fragment which specifically binds to the same antigenic
CC determinant as a monoclonal antibody chosen from HB20-1, HB20-3, HB20-4
CC and HB20-25 in a carrier), a cell line producing the mab, producing the
CC mab, an antigen binding fragment of the mab, an isolated nucleic acid
CC encoding a heavy chain or light chain comprising a variable region

CC (comprising CDR3, or CDR1, CDR2 and CDR3 regions from mAb chosen from
CC HB20-1, HB20-3, HB20-4, HB20-5, HB20-25, MB20-11, MB20-2, MB20-7,
CC MB20-8, MB20-10, MB20-11, MB20-14, MB20-16 and MB20-18) a vector
CC comprising the nucleic acid, a cell comprising the nucleic acid or
CC vector, and depleting B cells in a mammalian subject (involving
CC administering the mAb and anti-CD22 or anti-CD19 antibody). The anti-CD20
CC mAb, compositions and cells are useful for depleting B cells in a
CC mammalian subject and for treating a B cell disorder. The B cell disorder
CC is B cell malignancy or autoimmune disease e.g. rheumatoid arthritis,
CC idiopathic thrombocytopenic purpura or hemolytic anemia. The mammalian
CC subject is resistant to anti-CD20 mAb therapy or resistant to therapy
CC with mAb C2B8. The mammalian subject has been or is currently treated
CC with chemotherapy. The mammalian subject had a relapse in a B cell
CC disorder. The mammalian subject is immunocompromised. The present
CC sequence represents a CDR (complementarity determining region) from anti-
CC CD20 monoclonal antibody.

SQ Sequence 12 AA;

Query Match 37.5%; Score 27; DB 9; Length 12;
Best Local Similarity 45.5%; Pred. No. 8e+02; Mismatches 0; Gaps 0;
Matches 5; Conservative 4; Indels 2;

QY 4 SVAKSVKSLYL 14
||:|:|:|
Db 1 SVASNIRSNLYL 11

RESULT 34
AAG64140
ID AAG64140 standard; peptide; 15 AA.

AC AAG64140;

XX 25-SEP-2001 (first entry)

DE Ribosomal protein S17 10 N-terminal peptide.

XX Ribosomal protein S17 10; cancer; haemopathy; infection;
KM human immunodeficiency virus; HIV; immunological disease;
KW inflammatory disease; cytostatic; anti-HIV; anti-inflammatory;
KW immunomodulator.

XX Unidentified.

OS MO200146411-A1.

PN 28-JUN-2001.

XX 11-DEC-2000; 2000MO-CN000551.

PF 21-DEC-1999; 99CN-00125667.

XX (UYFU-) UNIV FUDAN.
PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Xie Y;
XX WPI; 2001-441673/47.

DR Ribosomal protein S17 10 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation.

XX Example 6; Page 18; 34pp; Chinese.

XX The invention relates to an isolated polypeptide of ribosomal protein S17
CC 10 comprising a fully defined 88 amino acid sequence given in the
CC specification, or its fragment, analogue or derivative. The polypeptide
CC and the polynucleotide encoding it are useful in the diagnosis and
CC treatment of malignant tumours, haemopathy, HIV infection, immunological
CC diseases and inflammatory diseases. The polypeptide is also useful for
CC screening mimics, agonists, antagonists or inhibitors, or for peptide

CC fingerprinting identification. The polynucleotide can be used to design
CC primers for nucleic acid amplification or to design probes for
CC hybridisation reactions, or in producing gene chips or microarrays. The
CC present sequence is the N-terminus of the polypeptide of the invention
XX

SQ Sequence 15 AA;

Query Match 37.5%; Score 27; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+03; Mismatches 0; Gaps 0;
Matches 5; Conservative 3; Indels 3;

QY 4 SVAKSVKSLYL 14
||:|:|:|
Db 5 TVVKSIKIFLYL 15

RESULT 35
ADG73517
ID ADG73517 standard; peptide; 15 AA.

AC ADG73517;

XX 11-MAR-2004 (first entry)

DE E faecalis methionine aminopeptidase type I (MAP) tryptic peptide 3.

XX (5-methylaminomethyl-2-thiouridylate)-methyltransferase; antibacterial;
KM bacterial infection; antimicrobial; disinfectant; soap; additive;
KW culture media; enzyme; tryptic digestion;
KM methionine aminopeptidase type I; MAP; map.

XX Enterococcus faecalis.

OS WO2003083099-A2.

PN 09-OCT-2003.

XX 02-APR-2003; 2003MO-CA000462.

PF 02-APR-2002; 2002US-0369511P.
PR 31-MAY-2002; 2002US-0385089P.
PR 04-JUN-2002; 2002US-0385751P.
PR 05-JUN-2002; 2002US-0386367P.
PR 05-JUN-2002; 2002US-0386553P.
PR 05-JUN-2002; 2002US-0386566P.
PR 05-JUN-2002; 2002US-0386577P.
PR 06-JUN-2002; 2002US-0386390P.
PR 06-JUN-2002; 2002US-0386601P.
PR 31-JUL-2002; 2002US-0399722P.
PR 05-NOV-2002; 2002US-0424053P.
PR 27-DEC-2002; 2002US-0436804P.
PR 27-DEC-2002; 2002US-0436834P.
PR 27-DEC-2002; 2002US-0436861P.
PR 31-DEC-2002; 2002US-0437281P.
PR 31-DEC-2002; 2002US-0437527P.

XX (AFFI-) AFFINIUM PHARM INC.

XX Edwards A, Dharamsi A, Vedadi M, Atrowsmith C, Awrey D;
XX Beattie B, Richards D, Domagala M, Houston S;
PI Mansoury K, Li O, Nethery K, Virag C, Ng I, Ouyang H, Tai M;
PI Thalakkad R, Kanagarajah D;
XX WPI; 2003-812543/76.

DR New isolated recombinant bacterial peptides, useful as targets for
XX antibacterial agents, also screening methods and host cells that express
PT them.

XX Disclosure; Fig 99; 369pp; English.

XX The invention relates to a novel isolated recombinant polypeptide that
CC has at least one of the biological activities of (5-methylaminomethyl-2-

CC thioninylate)-methyltransferase of *Staphylococcus aureus*. The
CC polypeptide of the invention demonstrates antibacterial activity and may
CC be useful for rational design of agents that may be utilized for treating
CC bacterial infections or as general antimicrobials, for example, as
CC disinfectants, soaps or additives for culture media. The current sequence
CC is that of the (5-methylaminomethyl-2-thioninylate)-methyltransferase-
CC related tryptic peptide of the invention.

XX
XX
SQ Sequence 15 AA;
Query Match 37.5%; Score 27; DB 7; Length 15;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
|:|:|:|
Db 1 KALYLG 6

RESULT 36
ADV22635
ID ADV22635 standard; peptide; 15 AA.
XX
XX ADV22635;
AC
XX
XX 10-MAR-2005 (first entry)
DE HIV-1 Rev protein, immunogenic peptide #14.
XX
XX Vaccine; virucide; antigen; autoimmune disease; infection;
XX immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
XX breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
XX pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
XX Hodgkin's lymphoma.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO2004108753-A1.
PN
XX
XX 16-DEC-2004.
PD
XX
XX 10-JUN-2004; 2004WO-AU000775.
PF
XX
XX 10-JUN-2003; 2003AU-00902875.
PR 25-MAR-2004; 2004AU-00901589.
XX
XX (UYME) UNIV MELBOURNE.
PA
XX
XX Kent SJ;
PI
XX
XX WPI; 2005-031657/03.
DR
XX
XX Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
XX
XX Disclosure; SEQ ID NO 1055; 645bp; English.

XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for modulating an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease

CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC or aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from an HIV-1
CC protein.

XX
XX
SQ Sequence 15 AA;
Query Match 37.5%; Score 27; DB 9; Length 15;
Best Local Similarity 41.7%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYLIG 15
|:|:|:|
Db 2 SISWILSTYLIG 13

RESULT 37
AEC11117
ID AEC11117 standard; peptide; 15 AA.
XX
XX AEC11117;
AC
XX
XX 20-OCT-2005 (first entry)
DE
XX
XX Enterococcus faecalis methionine aminopeptidase type I peptide.
XX protein purification; antibacterial; antimicrobial; infection;
XX drug screening; methionine aminopeptidase type I.
XX
XX Enterococcus faecalis.
OS
XX
XX US2005181388-A1.
PN
XX
XX 18-AUG-2005.
PD
XX
XX 04-OCT-2004; 2004US-00958216.
PF
XX
XX 02-APR-2002; 2002US-0369511P.
PR 04-APR-2002; 2002US-0369817P.
XX
XX 04-APR-2002; 2002US-0370102P.
PR 08-APR-2002; 2002US-0370778P.
XX
XX 08-APR-2002; 2002US-0370929P.
PR 08-APR-2002; 2002US-0370820P.
XX
XX 08-APR-2002; 2002US-0370859P.
PR 08-APR-2002; 2002US-0370915P.
XX
XX 09-APR-2002; 2002US-0371067P.
PR 09-APR-2002; 2002US-0371107P.
XX
XX 09-APR-2002; 2002US-0371140P.
PR 09-APR-2002; 2002US-0371185P.
XX
XX 31-MAY-2002; 2002US-0385089P.
PR 31-MAY-2002; 2002US-0385426P.
XX
XX 04-JUN-2002; 2002US-0385751P.
PR 05-JUN-2002; 2002US-0386018P.
XX
XX 05-JUN-2002; 2002US-0386367P.
PR 05-JUN-2002; 2002US-0386548P.

PR 05-JUN-2002; 2002US-0386553P.
 PR 05-JUN-2002; 2002US-0386566P.
 PR 05-JUN-2002; 2002US-0386577P.
 PR 06-JUN-2002; 2002US-0386283P.
 PR 06-JUN-2002; 2002US-0386399P.
 PR 06-JUN-2002; 2002US-0386430P.
 PR 06-JUN-2002; 2002US-0386601P.
 PR 06-JUN-2002; 2002US-0386826P.
 PR 06-JUN-2002; 2002US-0386869P.
 PR 31-JUL-2002; 2002US-039972P.
 PR 01-AUG-2002; 2002US-0400348P.
 PR 05-NOV-2002; 2002US-0424053P.
 PR 06-NOV-2002; 2002US-0424380P.
 PR 08-NOV-2002; 2002US-0424395P.
 PR 08-NOV-2002; 2002US-0425086P.
 PR 08-NOV-2002; 2002US-0425200P.
 PR 24-DEC-2002; 2002US-0436243P.
 PR 24-DEC-2002; 2002US-0436288P.
 PR 24-DEC-2002; 2002US-0436345P.
 PR 24-DEC-2002; 2002US-0436349P.
 PR 26-DEC-2002; 2002US-0436566P.
 PR 26-DEC-2002; 2002US-0436572P.
 PR 26-DEC-2002; 2002US-0436588P.
 PR 27-DEC-2002; 2002US-0436675P.
 PR 27-DEC-2002; 2002US-0436708P.
 PR 27-DEC-2002; 2002US-0436734P.
 PR 27-DEC-2002; 2002US-0436804P.
 PR 27-DEC-2002; 2002US-0436834P.
 PR 27-DEC-2002; 2002US-0436842P.
 PR 27-DEC-2002; 2002US-0436861P.
 PR 27-DEC-2002; 2002US-0436885P.
 PR 27-DEC-2002; 2002US-0436889P.
 PR 27-DEC-2002; 2002US-0436893P.
 PR 27-DEC-2002; 2002US-0436900P.
 PR 30-DEC-2002; 2002US-0436947P.
 PR 30-DEC-2002; 2002US-0436971P.
 PR 30-DEC-2002; 2002US-0436987P.
 PR 30-DEC-2002; 2002US-0437013P.
 PR 30-DEC-2002; 2002US-0437038P.
 PR 30-DEC-2002; 2002US-0437141P.
 PR 31-DEC-2002; 2002US-0437281P.
 PR 31-DEC-2002; 2002US-0437527P.
 PR 31-DEC-2002; 2002US-0437620P.
 PR 31-DEC-2002; 2002US-0437638P.
 PR 02-APR-2003; 2003WO-CA000462.
 PR 04-APR-2003; 2003WO-CA000464.
 PR 08-APR-2003; 2003WO-CA000481.
 PR 08-APR-2003; 2003WO-CA000485.

XX (AFFI-) AFFINIUM PHARM INC.

XX Edwards A, Dharamaji A, Vedadi M, Alam MZ, Arrowsmith C, Awrey DE;
 PI Beattie B, Buzadzija K, Canadien V, Domagala M, Houston S;
 PI Kanagarajah D, Li Q, Mansoury K, McDonald M, Nethery-Brooks K, Ng I;
 PI Ouyang H, Pinder B, Richards D, Tai M, Thalakada R, Vallee F;
 PI Virag C;

XX WPI; 2005-628189/64.

XX New composition comprising purified polypeptides from bacteria (e.g.
 PT Escherichia coli), useful for diagnosing, preventing or treating
 PT microbial infections, or in pharmacogenomic or drug screening procedures.
 XX
 PS Example 1; Fig 99; 667pp; English.

XX The invention relates to a composition (I) comprising purified
 CC polypeptides from bacteria. Also described: (1) a crystallized,
 CC recombinant polypeptide comprising an amino acid sequence of (I), where
 CC the polypeptide is in crystal form; (2) a crystallized complex comprising
 CC the crystallized, recombinant polypeptide and a co-factor or a small
 CC organic molecule, where the complex is in crystal form; and (3) a host
 CC cell comprising a nucleic acid encoding a polypeptide of (I), where a
 CC culture of the host cell produces at least about 1 mg of the polypeptide

CC per liter of culture and the polypeptide is at least about one-third
 CC soluble as measured by gel electrophoresis. The composition and methods
 CC are useful for diagnosing, preventing or treating diseases, such as
 CC microbial infections. These may also be used in pharmacogenomic or drug
 CC screening procedures. The present sequence represents a *Enterococcus*
 CC faecalis methionine aminopeptidase type I peptide, which is used in an
 CC example from the present invention.

XX Sequence 15 AA;

Query March 37.5%; Score 27; DB 9; Length 15;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 DB 1 KALYLG 6

RESULT 38

ID ADT73298 standard; peptide; 9 AA.

AC ADT73298;

DT 13-JAN-2005 (first entry)

DE Human RSV N high affinity binding peptide SegID 1194.

XX human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;

KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.

XX Human respiratory syncytial virus.

XX WO2004092207-A2.

PD 28-OCT-2004.

PF 16-APR-2004; 2004WO-EP004061.

XX 16-APR-2003; 2003EP-00447095.

XX (ALGO-) ALGONOMICS NV.

PI Lasters I, Deemert J, Stegmann T;

DR WPI; 2004-758334/74.

XX New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
 PT or P) for inducing an immune response to RSV or for diagnosing,
 PT preventing or treating viral infections, particularly RSV infection.

XX Claim 11; SEQ ID NO 1194; 143pp; English.

XX This invention relates to novel isolated or purified peptides of the
 CC human respiratory syncytial virus (RSV), in particular ten RSV genes
 CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
 CC known as the IC protein) & NS-2 (1B protein), a polymerase protein L and
 CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
 CC SH (also known as the 1A protein). Specifically, it refers to a
 CC composition comprising an above peptide mixed with a pharmaceutical
 CC excipient or an RSV immunogenic composition comprising a recombinant
 CC expression vector with a nucleic acid insert encoding an above peptide.
 CC The present invention describes an in vitro method of detecting cytotoxic
 CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
 CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
 CC RSV peptide is useful for preparing a diagnostic composition or an RSV
 CC (prophylactic or therapeutic) vaccine composition for a DNA-based
 CC immunisation, or for preparing an immune response provoking vaccine in
 CC the event of RSV infection (the vaccine being prepared by contacting the
 CC polypeptide in an immune response-provoking amount of specific CTL).
 CC Accordingly, these peptide compositions have virucidal activity. This
 CC peptide sequence is a human RSV high binding affinity peptide of the

CC invention.
XX
SQ Sequence 9 AA;
Query Match 36.1%; Score 26; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.1e+06;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 VAKSVKSL 12
:|||||:
DB 2 LAKSVKNI 9
RESULT 39
ADT73299
ID ADT73299 standard; peptide; 9 AA.
XX
AC ADT73299;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV N high affinity binding peptide Segid 1195.
XX
KM human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP04061.
XX
PR 16-APR-2003; 2003EP-0047095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 11; SEQ ID NO 1195; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 36.1%; Score 26; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.1e+06;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 VAKSVKSL 12
:|||||:
DB 1 LAKSVKNI 8
RESULT 40
ADK40048
ID ADK40048 standard; peptide; 10 AA.
XX
AC ADK40048;
XX
DT 06-MAY-2004 (first entry)
XX
DE PNA molecule-related transporter peptide #220.
XX
KM modified peptide nucleic acid; PNA; TP-L-PNA; TP; transporter peptide; L;
KM bond; linker; antibacterial; antimicrobial; cytostatic; virucide;
KM immunosuppressive; antisense-therapy; infectious disease;
KM bacterial infection; disinfection; cancer; bacterial; viral infection;
KM metabolic disease; immunological disorder.
XX
OS Unidentified.
XX
PN WO2003092736-A2.
XX
PD 13-NOV-2003.
XX
PF 01-MAY-2003; 2003WO-DK000280.
XX
PR 01-MAY-2002; 2002DK-0000661.
XX
PA (PANT-) PANTHECO AS.
XX
PI Tolborg J, Frandsen TP, Nielsen BR, Johansen C, Kjærulff S;
XX
DR WPI; 2004-011826/01.
XX
PT New modified peptide nucleic acid (PNA) molecule, useful in treating
PT and/or preventing cancer, viral infections, metabolic diseases,
PT immunological disorders, and in particular bacterial infections.
XX
PS Claim 6; Page 84; 96pp; English.
XX
CC This invention relates to a novel modified peptide nucleic acid (PNA)
CC molecule. The invention comprises TP-L-PNA where TP transporter peptide;
CC L bond or a linker; PNA an oligomer of 4-35 monomers. The invention may
CC be useful for the development of compounds with an antibacterial,
CC antimicrobial, cytostatic, virucide or immunosuppressive. In addition,
CC the disclosed sequences could be used for antisense-therapy. The
CC compounds of the PNA molecule are useful in medicine, in particular for
CC the inactivation of the expression of specific genes by targeting the
CC genes at the mRNA, sRNA or DNA level. The PNA sequence is useful in the
CC treatment and/or prevention of infectious diseases, particularly
CC bacterial infections, or in disinfection of non-living objects. The
CC methods and compositions of the present invention are also useful for
CC treating cancer, bacterial and viral infections, metabolic diseases and
CC immunological disorders. The present sequence is that of a transporter
CC peptide which may be used during the creation of a PNA molecule of the
CC invention.
XX
SQ Sequence 10 AA;
Query Match 36.1%; Score 26; DB 8; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 FSVKSVK 10
:|||||:
DB 3 FKVAKVK 10

RESULT 41
ABJ36740
ID ABJ36740 standard; peptide; 11 AA.
AC
XX ABJ36740;
XX
DT 01-MAY-2003 (first entry)
XX
XX
DE G protein coupled receptor related peptide SEQ ID NO 81.
XX
XX Nootropic; cardiant; antiarteriosclerotic; hypotensive; cyostatic;
KM antibacterial; analgesic; antiallergic; antiaesthetic; antiinflammatory;
KM osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;
KM G protein coupled receptor signaling inhibitor; GPCR; library;
KM high throughput screening assay; stroke; myocardial infarction;
KM restenosis; atherosclerosis; hypertension; cancer; infection; asthma;
KM septic shock; pain; allergic disorder; inflammatory bowel disease;
KM osteoporosis; obesity; psychiatric; neurological disorder; anxiety;
KM schizophrenia; Alzheimer's disease.
XX
XX Caenorhabditis elegans.
OS
XX
XX WO200272778-A2.
PN
XX
XX 19-SEP-2002.
PD
XX
XX 14-MAR-2002; 2002WO-US007561.
PF
XX
XX 14-MAR-2001; 2001US-0275472P.
PR
XX 11-MAY-2001; 2001US-00852910.
PR
XX
XX (CUEB-) CUE BIOTECH.
PA
XX
XX Gilchrist A, Hamm HE;
PI
XX WPI; 2003-247841/24.
DR
XX
XX Identifying G protein coupled receptor (GPCR) signaling inhibitors,
PT useful in screening drugs for treating stroke, cancers or pain, by
PT identifying compounds that block GPCR mediated signaling with high
PT affinity and specificity.
XX
XX
XX Claim 94; Page 25; 94pp; English.
PS
XX
XX The invention relates to a novel method for identifying a G protein
CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
CC selecting or identifying a member of a library of peptides and/or
CC candidate compounds, having binding to a GPCR of higher affinity than
CC that of the native peptide. The peptide library is based on a native GPCR
CC binding peptide. The method is useful for identifying inhibitors of a G
CC protein coupled receptor (GPCR) signaling. The method is particularly
CC useful for identifying drugs that antagonise the binding between a GPCR
CC and its extracellular ligand(s). The method is especially useful in
CC modern high throughput screening assays for identifying potent lead
CC compounds. The compounds, peptides or inhibitors identified by the method
CC are useful for preventing, ameliorating or treating diseases in which
CC GPCR signaling is a causative factor or in which a specific class of G
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
CC atherosclerosis, hypertension, cancers, infections, septic shock, pain,
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
CC obesity, or psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
CC relating to the G protein coupled receptors of the invention
XX
XX
XX Sequence 11 AA;

Query Match 36.1%; Score 26; DB 6; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 5 VAKSVKSLYL 14
:|:|:|:|:
DB 1 IAKNLKSMGL 10

RESULT 42
ADT51155
ID ADT51155 standard; peptide; 11 AA.
AC
XX ADT51155;
XX
DT 13-JAN-2005 (first entry)
XX
XX
DE G protein coupled receptor signalling modifying peptide #62.
XX
XX cerebroprotective; vasotropic; cardiant; antiarteriosclerotic;
KM hypotensive; cyostatic; antibacterial; fungicide; virocidic; analgesic;
KM antiallergic; antisthmatic; antiinflammatory; antiparkinsonian;
KM neuroprotective; nootropic; gene therapy; G protein coupled receptor;
KM GPCR; signaling modifying peptide; stroke; myocardial infarction;
KM atherosclerosis; hypertension; cancer; infection; pain; allergy; asthma;
KM inflammation; Parkinson's disease; Alzheimer's disease.
XX
XX
XX Synthetic.
OS
XX
XX WO2004092199-A2.
PN
XX
XX 28-OCT-2004.
PD
XX
XX 12-APR-2004; 2004WO-US011167.
PF
XX
XX 11-APR-2003; 2003US-00411336.
PR
XX
XX (CUEB-) CUE BIOTECH INC.
PA
XX
XX Gilchrist A, Hamm HM;
PI
XX WPI; 2004-766826/75.
DR
XX
XX Identifying modulators of G protein coupled receptor (GPCR) signaling,
PT useful for treating diseases associated with altered GPCR signaling (e.g.
PT stroke), comprises screening a peptide library for high affinity binding
PT to the GPCR.
XX
XX
XX Disclosure; SEQ ID NO 81; 264pp; English.
PS
XX
XX The invention relates to a method of identifying a G protein coupled
CC receptor (GPCR) signaling modifying peptide by providing a peptide
CC library based on a native GPCR binding peptide, screening the peptide
CC library for high affinity binding to the GPCR, and selecting a member of
CC the peptide library having binding to the GPCR of higher affinity than
CC that of the native peptide. The composition and methods are useful for
CC identifying modulators of GPCR signaling, for modulating the activity of
CC GPCR or for drug designing. These may be used for diagnosing, preventing
CC or treating diseases associated with altered GPCR signaling, such as
CC stroke, myocardial infarction, atherosclerosis, hypertension, cancer,
CC infections (e.g. bacterial, fungal or viral), pain, allergies, asthma,
CC inflammation, Parkinson's disease and Alzheimer's disease. This sequence
CC corresponds to a peptide of the invention.
XX
XX
XX Sequence 11 AA;

Query Match 36.1%; Score 26; DB 8; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 5 VAKSVKSLYL 14
:|:|:|:|:
DB 1 IAKNLKSMGL 10

RESULT 43
AAR68663
ID AAR68663 standard; peptide; 12 AA.
AC
XX AAR68663;

XX 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-SEP-1995 (first entry)
XX
DE T cell epitope derived from V3 isolate SF2.
XX
KM T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;
KW pol; vaccine; multimeric peptide; AIDS; 3D organisation.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9429339-A1.
XX
PD 22-DEC-1994.
XX
PF 08-JUN-1994; 94WO-CN000317.
XX
PR 09-JUN-1993; 93US-00073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Sia CDY, Chong P, Klein MH;
XX
DR WPI; 1995-036400/05.
XX
PT Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of
PT gag protein linked to B-cell epitope of V3 loop protein of an HIV-1
XX isolate.
XX
PS Disclosure; Page 39; 69pp; English.
XX
CC This sequence represents a T-cell epitope derived from the V3 sequence of
CC the HIV-1 isolate SF2, which may be linked to a B-cell epitope from the
CC V3 (MN) loop from HIV-1. These chimeric peptides may then be used in the
CC production of HIV-1 vaccines. These peptide sequences may also be used in
CC the production of multimeric peptides in which the peptides are C-
CC terminally modified by the addition of a lys residue which is modified on
CC its epsilon amino acid to carry an additional copy of the peptide
CC molecule. The linear and multimeric peptides may be used for the
CC treatment of AIDS by acting to displace the binding of HIV virus to human
CC or animal cells or by disturbing the 3D organisation of the virus.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 10 KSLYLIG 15
||:|:|
DB 2 KSIYIG 7
XX
RESULT 44
AAW25833
ID AAW25833 standard; peptide; 12 AA.
XX
AC AAW25833;
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1997 (first entry)
XX
DE HIV B-cell strain SF2 env protein V3 loop peptide.
XX
KM HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
KW V3 loop; vaccine; determinant; chimaeric.
OS Synthetic.
XX
PN US5639854-A.
XX

XX 17-JUN-1997.
PD 09-JUN-1994; 94US-00257528.
XX
PF 09-JUN-1993; 93US-00073378.
XX
PR 09-JUN-1993; 93US-00073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Klein MH, Sia CDY, Chong P;
XX
DR WPI; 1997-332082/30.
XX
PT Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag
PT protein T-cell epitope linked to env protein B-cell epitope.
XX
PS Disclosure; Col 21; 41pp; English.
XX
CC The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIB, RF, Z6, 2054,
CC 1714 and BX08. The peptides are chimaeric and can be linked to a branched
CC lys backbone. This sequence represents the B-cell env protein V3 loop
CC peptide from HIV-1 strain SF2. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 10 KSLYLIG 15
||:|:|
DB 2 KSIYIG 7
XX
RESULT 45
AAW67349
ID AAW67349 standard; peptide; 12 AA.
XX
AC AAW67349;
XX
DT 17-OCT-2003 (revised)
DT 25-JAN-1999 (first entry)
XX
DE HIV-1 strain SF2 gp120 V3 loop epitope peptide.
XX
KM Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
KW V3 loop.
XX
OS Human immunodeficiency virus 1.
XX
PN US5817754-A.
XX
PD 06-OCT-1998.
XX
PF 05-JUN-1995; 95US-00464329.
XX
PR 09-JUN-1993; 93US-00073378.
PR 09-JUN-1994; 94US-00257528.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Chong P, Klein MH, Sia CDY;
XX
DR WPI; 1998-556461/47.
XX

PT Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
 PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
 XX
 PS Disclosure; Col 21; 40pp; English.
 CC
 CC The invention relates to a novel immunogenic composition for use in
 CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
 CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
 CC are generally designed based on the p24 core protein and the B-cell
 CC epitopes from the V3 loop of the gp120 protein from various HIV-1
 CC strains. This peptide represents the V3 loop epitope from the HIV-1
 CC strain SF2. (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 12 AA;
 Query Match 36.1%; Score 26; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 10 KSLYLIG 15
 ||:|:
 ||:|:
 Db 2 KSIYIG 7
 RESULT 46
 AAU99957
 ID AAU99957 standard; peptide; 12 AA.
 XX
 AC AAU99957;
 XX
 DT 05-MAY-1999 (first entry)
 XX
 DE HIV-1 vaccine synthetic peptide SEQ ID NO.34.
 XX
 KM HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
 XX gag protein; B-cell epitope; gp1 protein; chimeric; infection.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 PN US5876731-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 05-JUN-1995; 95US-00462507.
 XX
 PR 09-JUN-1993; 93US-00073378.
 PR 09-JUN-1994; 94US-00257528.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Chong P, Klein MH, Sia CDY;
 XX
 DR WPI; 1999-189590/16.
 XX
 PT Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
 PT epitope linked to gp1 B-cell epitope.
 XX
 PS Example 1; Col 41-42; 41pp; English.
 XX
 CC The present invention describes a synthetic peptide comprising an amino
 CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
 CC its C terminus to an amino acid sequence containing a B-cell epitope of
 CC an HIV gp1 protein and containing the amino acid sequence: X1KDX2;
 CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
 CC capable of eliciting an HIV-specific antiserum and recognizing the
 CC sequence X1KDX2. The synthetic peptide is useful in vaccines against
 CC HIV infection and in diagnostic applications. AAU98892 to AAU98906, and
 CC AAU98899 to AAU98989 represent synthetic peptides from the present
 CC invention
 CC
 XX
 SQ Sequence 12 AA;

Query Match 36.1%; Score 26; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 10 KSLYLIG 15
 ||:|:
 ||:|:
 Db 2 KSIYIG 7
 RESULT 47
 AAU9755
 ID AAU9755 standard; peptide; 12 AA.
 XX
 AC AAU9755;
 XX
 DT 17-OCT-2003 (revised)
 DT 26-NOV-1999 (first entry)
 XX
 DE HIV1 chimeric peptide V3-SF2.
 XX
 KM HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope;
 XX infection; antibody; antiviral.
 XX
 OS Human immunodeficiency virus 1.
 OS
 PN US5951966-A.
 XX
 PD 14-SEP-1999.
 XX
 PE 06-JUN-1995; 95US-00467881.
 XX
 PR 09-JUN-1993; 93US-00073378.
 PR 09-JUN-1994; 94US-00257528.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Klein MH, Chong P, Sia CDY;
 XX
 DR WPI; 1999-550482/46.
 XX
 PT Immunogenic composition containing synthetic fusion polypeptides
 PT containing both the T and B cell epitopes of the human immunodeficiency
 PT virus, useful antigens in producing vaccines.
 XX
 PS Example 1; Col 22; 43pp; English.
 XX
 CC This sequence represents a fragment of a HIV1 protein, and can be used in
 CC the immunogenic composition of the invention. The composition comprises a
 CC synthetic fusion polypeptide which includes a sequence encoding 1 or more
 CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
 CC carrier. Both the T cell and B cell epitopes are derived from HIV
 CC proteins. The compositions are useful as vaccines against HIV infection.
 CC The composition induces HIV-1-specific polyclonal antibodies that are
 CC opsonising and antiviral. The peptide components may be selected to
 CC induce a response against different viral isolates and in subjects who
 CC recognise different T cell epitopes. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 12 AA;
 Query Match 36.1%; Score 26; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 10 KSLYLIG 15
 ||:|:
 ||:|:
 Db 2 KSIYIG 7
 RESULT 48
 AAU70355
 ID AAU70355 standard; peptide; 12 AA.
 XX

AC	AATU0355;
AD	
DT	14-FEB-2002 (first entry)
XX	
DE	Mouse Kappa IV light chain CDR1.
XX	
KW	Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW	complementarity determining region; framework region; IGBP;
KW	transgenic plant; immunoglobulin binding protein array; IGM; Igg; IGA;
Igd; Igb; IgY; Igm; kappa; lambda; CHBP.	
OS	Mus musculus.
XX	
PN	WO200183806-A1.
PD	
PD	08-NOV-2001.
PX	
PF	02-MAY-2001; 2001WO-US014349.
PR	
PR	02-MAY-2000; 2000US-00563222.
XX	
PA	(EPIC-) EPICYTE PHARM INC.
PI	
XX	Hiact AC, Hein MB;
XX	
DR	WPI; 2002-055482/07.
XX	
PT	Preparing immunoglobulin binding protein array in plant cells by
PT	transforming the cells with different polynucleotides encoding binding
PT	protein polypeptides specific to ligand, selecting plant cells for
PT	preparing array.
XX	
PS	Disclosure; Page 14; 123pp; English.
XX	
CC	The invention relates to transforming a population of cells (e.g. plant
CC	cells) comprising using a library of two different polynucleotides
CC	encoding different immunoglobulin binding protein (IGBP) polypeptides
CC	that specifically bind to a ligand or form one or more disulfide bonds
CC	with polypeptides in transfected cells, to generate an IGBP that binds to
CC	a ligand, and transformed plant cells are selected, and preparing ah IGBP
CC	array in plant cells. At least one peptide sequence has at least 75%
CC	sequence identity to a framework region (FR) of a native Igm, Igd, Iga,
CC	Igd, Ige, Igy, kappa or lambda immunoglobulin molecule. The method is
CC	useful for preparing an immunoglobulin binding protein array, preferably
CC	heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC	plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC	cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC	discovery of e.g. screening assays of IGBPs having desired
CC	characteristics. The present sequence is a mammalian immunoglobulin
CC	derived peptide that may be incorporated into an IGBP of the invention
XX	
SQ	Sequence 12 AA;
XX	
Query Match	36.1%; Score 26; DB 5; Length 12;
Best Local Similarity	54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative	1; Mismatches 4; Indels 0; Gaps 0
Oy	4 SVAKSVKSLYL 14 : 1 SASSSVSSSYL 11
Db	
RESULT 49	
ADE25804	
ID	ADE25804 standard; peptide; 12 AA.
XX	
AC	ADE25804;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Anti-alpha-v-beta-6 monoclonal antibody light chain CDR1 SEQ ID NO:11.
KW	monoclonal antibody; alpha-v-beta-6; latency associated peptide; LMP;

XX	cytostatic; dermatological; vulnary; hepatotropic; immunosuppressive;
KM	vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
XX	kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
XX	Synthetic.
OS	WO2003100033-A2.
PN	
XX	
PD	
XX	
PF	13-MAR-2003; 2003WO-US008048.
PR	13-MAR-2002; 2002US-0364991P.
XX	13-NOV-2002; 2002US-0426286P.
XX	
PA	(BIOT) BIOGEN INC.
PI	(REGC) UNIV CALIFORNIA.
DR	Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
XX	WPI; 2004-035139/03.
XX	
PT	New monoclonal antibody that specifically binds to alpha-v-beta-6, and
PT	inhibits the binding of alpha v beta 6 to latency associated peptide
PT	(LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
XX	syndrome.
PS	Claim 13; SEQ ID NO 11; 83pp; English.
XX	
XX	The present invention describes a monoclonal antibody (I) that
CC	specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
CC	-beta-6 to latency associated peptide (LAP) with an IC50 value lower than
CC	that of 1005. Also described: (1) an anti-alpha-v-beta-6 antibody
CC	comprising heavy chain complementarity determining regions (CDR) 1, 2,
CC	and 3, or a heavy and light chain variable domain sequence; (2) a
CC	monoclonal antibody that specifically binds to alpha-v-beta-6 but does
CC	not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
CC	preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
CC	comprising the antibody and a carrier; (4) a method for treating a
CC	subject having or at risk of having a disease mediated by alpha-v-beta-6
CC	by administering to the subject the composition described above, and so
CC	alleviating or postponing the onset of the disease; (5) a method of
CC	detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
CC	sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
CC	6.2B1, 7.1G10, 7.7G5, or 7.1CX, which respectively comprises American
CC	Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
CC	3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytostatic,
CC	dermatological, vulnary, hepatotropic and immunosuppressive activities,
CC	and can be used in vaccines. The antibodies, compositions and methods of
CC	the present invention can be used for preventing or treating a disease
CC	mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
CC	liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
CC	preferably epithelial cancer, oral, skin, cervical, pharyngeal,
CC	laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
CC	Alport's syndrome. The present sequence is used in the exemplification of
CC	the present invention.
XX	
XX	
SQ	Sequence 12 AA;
XX	
XX	
QY	Query Match 36.1%; Score 26; DB 8; Length 12;
DB	Best Local Similarity 54.5%; Pred. No. 1.2e+03;
XX	Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0
XX	
XX	4 SVANSVKSLEYL 14
XX	: - - -
XX	1 SASSSVSSSYL 11
XX	
XX	RESULT 50
ID	ADHS9661 standard; peptide; 12 AA.
XX	ADHS9661;
AC	ADHS9661;

XX 25-MAR-2004 (first entry)
DT Light chain CDR-1 peptide.
XX
DE MUC1; mucin; cytostatic; malignancy; cancer; CDR.
XX
KW Unidentified.
XX
OS WO2003106497-A1.
XX
PN 24-DEC-2003.
XX
PD 16-JUN-2003; 2003WO-GB002585.
XX
PF 14-JUN-2002; 2002US-0388313P.
XX
PR (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCA/ J D.
XX
PI Gold DV, Goldenberg DM, Hansen H;
XX
DR WPI; 2004-156341/15.
XX
XX Novel tumor-associated PAM4 antibody binding a domain located between
PT amino terminus and start of repeat domain of MUC1, derived by
PT immunization and/or selection with mucin, useful for treating pancreatic
PT cancer.
XX
PS Claim 5; SEQ ID NO 1; 110pp; English.
XX
SQ The present invention relates to an antibody or its fragment binding a
CC domain located between the amino terminus and the start of a repeat
CC domain of MUC1, derived by immunization and/or selection with mucin. The
CC method is useful for treating a malignancy in a subject, for delivering a
CC diagnostic/detection agent, a therapeutic agent, or its combination to a
CC target, for diagnosing or treating cancer, which involves administering
CC the antibody to a subject. The cancer is a pancreatic cancer. The method
CC can be used for intraoperative identification of diseased tissues,
CC endoscopic identification of diseased tissues or intravascular
CC identification of diseased tissues. The method is useful for treating a
CC cancer cell in a subject. The present sequence represents a complementary
CC determining region of the invention.
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 8; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 4 SVAKSVKSYL 14
| : | | | |
Db 1 SASSSVSSYL 11
XX
RESULT 51
ADH59682
ID ADH59682 standard; peptide; 12 AA.
XX
AC ADH59682;
XX
DT 25-MAR-2004 (first entry)
XX
XX Light chain CDR1.
DE
XX PAM4 humanized; hPAM4; Cytostatic; Immunotherapy; cancer; CDR.
KW Homo sapiens.
XX
OS WO2003106495-A2.
XX
PN 24-DEC-2003.
XX
PR

PF 16-JUN-2003; 2003WO-GB002593.
XX
XX 14-JUN-2002; 2002US-0388314P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCA/ J D.
XX
PI Goldenberg DM, Hansen H, Qu Z;
XX
DR WPI; 2004-156340/15.
XX
XX Novel PAM4 humanized antibody or its fragment that binds to domain
PT located between amino terminus and start of repeat domain of MUC1, useful
PT for treating pancreatic cancer.
XX
XX Claim 6; SEQ ID NO 1; 109pp; English.
XX
XX The present invention relates to a PAM4 humanized (hPAM4) antibody or its
CC fragment that binds to the domain located between the amino terminus and
CC start of the repeat domain of MUC1, where the antibody is derived by
CC immunization and/or selection with mucin. The antibody is useful for
CC diagnosing or treating cancer, preferably pancreatic cancer, is useful
CC for treating a malignancy in a subject, is useful for treating a cancer
CC cell in a subject, is useful for detection of lesions during an
CC endoscopic, intravascular catheter, or surgical procedure, is also useful
CC for close-range lesion detection, during an operative, intravascular, or
CC endoscopic procedure. The antibody is efficiently useful in diagnosing
CC and treating pancreatic cancer. The present sequence represents a light
CC chain complementary determining region (CDR).
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 8; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 4 SVAKSVKSYL 14
| : | | | |
Db 1 SASSSVSSYL 11
XX
RESULT 52
ADD90504
ID ADD90504 standard; protein; 14 AA.
XX
AC ADD90504;
XX
DT 29-JAN-2004 (first entry)
XX
XX Novel human secreted protein seq id 68 protein feature seq id 319.
DE
XX gene therapy; cytostatic; cancer; human; secreted protein.
KW Homo sapiens.
XX
OS US2003199683-A1.
XX
PN 23-OCT-2003.
XX
PD 30-MAR-2001; 2001US-00820649.
XX
PF 30-JUL-1997; 97US-0054209P.
XX
PR 30-JUL-1997; 97US-0054211P.
XX
PR 30-JUL-1997; 97US-0054212P.
XX
PR 30-JUL-1997; 97US-0054213P.
XX
PR 30-JUL-1997; 97US-0054215P.
XX
PR 30-JUL-1997; 97US-0054217P.
XX
PR 30-JUL-1997; 97US-0054218P.
XX
PR 30-JUL-1997; 97US-0054234P.
XX
PR 30-JUL-1997; 97US-0054236P.
XX
PR 18-AUG-1997; 97US-0055968P.
XX
PR 18-AUG-1997; 97US-0055969P.

PR 18-AUG-1997; 97US-0055972P.
 PR 19-AUG-1997; 97US-0056534P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056544P.
 PR 19-AUG-1997; 97US-0056561P.
 PR 19-AUG-1997; 97US-0056727P.
 PR 19-AUG-1997; 97US-0056729P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 29-JUL-1998; 98WO-US015949.
 PR 26-JAN-1999; 99US-00236557.
 PR 21-SEP-2000; 2000US-00666987.
 XX
 PA (RUBEN/) RUBEN S M.
 PA (FENG/) FENG P.
 PA (LAFLEUR/) LAFLEUR D W.
 PA (MOORE/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (KYAM/) KYAM H.
 PA (LIY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (CARTER/) CARTER K C.
 PA (ENDRESS/) ENDRESS G A.
 PA (WEIY/) WEI Y.
 PA (FANP/) FAN P.
 PA (ROSEN/) ROSEN C A.
 PI Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
 DR MPI; 2003-852813/79.
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g., cancer.
 XX
 PS Disclosure; SEQ ID NO 319; 213pp; English.
 XX
 CC The invention describes novel isolated human nucleic acids. The nucleic
 CC acid is useful for preparing a medicament for preventing, treating or
 CC ameliorating a medical condition e.g., cancer, and in gene therapy. This
 CC is the amino acid sequence of polypeptide feature of a novel human
 CC secreted protein of the invention.
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 36.1%; Score 26; DB 7; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PFSVAKSV 9
 Db 3 PFSISYSI 10
 XX
 RESULT 53
 ADG90323
 ID ADG90323 standard; peptide, 14 AA.
 AC ADG90323;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human secreted protein gene 58 extra polypeptide #1.
 XX
 KW Secretd protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW Rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.
 XX
 OS Homo sapiens.

XX
 PN US200316541-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 04-JUN-2002; 2002US-00160162.
 XX
 PR 30-JUL-1997; 97US-0054209P.
 PR 30-JUL-1997; 97US-0054211P.
 PR 30-JUL-1997; 97US-0054212P.
 PR 30-JUL-1997; 97US-0054213P.
 PR 30-JUL-1997; 97US-0054214P.
 PR 30-JUL-1997; 97US-0054215P.
 PR 30-JUL-1997; 97US-0054217P.
 PR 30-JUL-1997; 97US-0054218P.
 PR 30-JUL-1997; 97US-0054234P.
 PR 30-JUL-1997; 97US-0054236P.
 PR 18-AUG-1997; 97US-0055968P.
 PR 18-AUG-1997; 97US-0055969P.
 PR 18-AUG-1997; 97US-0055972P.
 PR 19-AUG-1997; 97US-0056534P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056544P.
 PR 19-AUG-1997; 97US-0056561P.
 PR 19-AUG-1997; 97US-0056727P.
 PR 19-AUG-1997; 97US-0056729P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 29-JUL-1998; 98WO-US015949.
 PR 26-JAN-1999; 99US-00236557.
 PR 05-JUN-2001; 2001US-0295558P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
 DR MPI; 2003-874923/81.
 XX
 PT Nucleic acids encoding 83 secreted polypeptides, useful for preventing,
 PT diagnosing and treating disorders related to their aberrant expression
 PT and activity.
 XX
 PS Disclosure; SEQ ID NO 319; 308pp; English.
 XX
 SQ
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences; a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment; a
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular

CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis
 CC thyroiditis, anemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 83 disclosed secreted protein genes.
 XX
 SO Sequence 14 AA;
 Query Match 36.1%; Score 26; DB 7; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PFSVAKSV 9
 |||::|:
 Db 3 PFSISYSI 10
 RESULT 54
 ID ADU83344 standard; peptide; 14 AA.
 XX
 AC ADU83344;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE NKkappa B-associated protein AD037 immunogenic peptide.
 XX
 KM Nuclear factor kappa B; NFkappaB; immunogen; inflammation;
 KM cardiovascular disease; neoplasia; gastrointestinal disease;
 KM immune disorder; immune deficiency; dermatological disease; infection;
 KM nutritional disorder; cerebrovascular ischemia; endocrine disease;
 KM injury; respiratory disease; gynecology and obstetrics; Kawasaki disease;
 KM rheumatic fever; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004100886-A2.
 XX
 PD 25-NOV-2004.
 XX
 PF 06-MAY-2004; 2004WO-US014279.
 XX
 PR 07-MAY-2003; 2003US-00431096.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Carman J, Feder JM, Nadler SG;
 XX
 DR WPI, 2005-047909/05.
 XX
 PT New nucleic acid molecule encoding an NFkappaB associated molecule,
 PT useful for diagnosing, preventing, treating, or ameliorating a medical
 PT condition, e.g. cancer, wounds, or immune, inflammatory, hepatic, viral
 PT or pulmonary disorder.
 XX
 PS Example 7; SEQ ID NO 289; 646bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule having
 CC NFkappaB (nuclear factor kappa B) modulating activity (or its fragments,
 CC variants, homologs and sequences hybridizing to it). Also included are an
 CC isolated polypeptide capable of modulating an NFkappaB response (or its
 CC domain, epitope, variant, species homolog or interacting protein), an
 CC isolated antibody that binds specifically to the isolated polypeptide, a
 CC method for preventing (treating, or ameliorating) a medical condition, a
 CC method of diagnosing a NFkappaB associated condition (or a susceptibility
 CC to a NFkappaB associated condition) in a subject, a method for
 CC identifying a binding partner to the polypeptide, a method of identifying
 CC a compound that modulates the biological activity of a NFkappaB

CC associated molecule, a method of screening for a compound that is capable
 CC of modulating the biological activity of a NFkappaB associated molecule
 CC and a compound that modulates the biological activity of a human NFkappaB
 CC associated molecule as identified by any of the methods above. The
 CC nucleic acid molecule and polypeptides, composition and methods are
 CC useful for diagnosing, preventing, treating, or ameliorating a medical
 CC condition, e.g. immune disorder, an inflammatory disorder in which
 CC polypeptides of the present invention are associated with the disorder
 CC either directly or indirectly, an inflammatory disorder related to
 CC aberrant NFkappaB regulation, a cancer, aberrant apoptosis, hepatic
 CC disorders, Hodgkins lymphomas, hematopoietic tumors, hyper-IGM syndromes,
 CC hypohydrotic ectodermal dysplasia, X-linked anhidrotic ectodermal
 CC dysplasia, immunodeficiency, albinism, influenza, viral
 CC HIV-1, hepatitis B, hepatitis C, EBV, influenza, viral
 CC replication, host cell survival, and evasion of immune responses,
 CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
 CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAB,
 CC autoimmune disorders, disorders related to hyper immune activity,
 CC disorders related to aberrant acute phase responses, hypercongenital
 CC conditions, birth defects, necrotic lesions, wounds, organ transplant
 CC rejection, conditions related to organ transplant rejection, disorders
 CC related to aberrant signal transduction, proliferating disorders, HIV
 CC propagation in cells infected with other viruses, associated with EL-8,
 CC disorders associated with aberrant IL-8 expression, disorders associated
 CC with aberrant IL-8 activity, pulmonary disorders, pulmonary fibrosis,
 CC Behcet's disease, bacterial infections, gynecological diseases,
 CC psoriasis, IGA nephropathy, chronic obstructive pulmonary disease,
 CC Kawasaki disease, Cronin's disease, peripheral arterial occlusive disease,
 CC Hodgkin's disease, idiopathic intermediate uveitis, hyaline membrane
 CC disease, acute rheumatic fever, chronic rheumatic heart disease,
 CC ulcerative colitis, autoimmune disorders, and autoimmune thyroid disease.
 CC The present sequence is an immunogenic peptide from the NFkappa B
 CC modulating protein AD037.
 XX
 SQ Sequence 14 AA;
 Query Match 36.1%; Score 26; DB 9; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVK 10
 |||::|:
 Db 1 VPISDSKSIQ 10
 RESULT 55
 ID ADY25663 standard; peptide; 14 AA.
 XX
 AC ADY25663;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Novel human secreted protein-related peptide SegIDJ319.
 XX
 KM cancer; cytostatic; arthritis; antiarthritic; asthma; antiasthmatic;
 KM acquired immune deficiency syndrome; rheumatoid arthritis; autoimmune;
 KM inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.;
 KM sepsis; antibacterial; immunosuppressive; acne; antiseborrheic;
 KM dermatological; psoriasis; antipsoriatic; atherosclerosis;
 KM antiarteriosclerotic; cerebrovascular ischemia; cerebroprotective;
 KM vasotropic; thrombosis; wound healing; vulnery; Alzheimers disease;
 KM neuroprotective; nocrotic; parkinsons disease; antiparkinsonian; autism;
 KM obsessive-compulsive disorder; tranquilizer; graft versus host disease;
 KM immune disorder; hematological disease; inflammation; infection;
 KM hyperproliferative disorders; renal disease; nephrotropic;
 KM cardiovascular disease; cardiovascular-gen.; respiratory disorder;
 KM neurological disease; neuroprotective; endocrine disease;
 KM reproductive disorders (general); gynecological.
 XX
 OS Homo sapiens.
 XX
 PN US2005037467-A1.

XX 17-FEB-2005.
 PD 09-SEP-2004; 2004US-00936773.
 XX 30-JUL-1997; 97US-0054209P.
 XX 30-JUL-1997; 97US-0054211P.
 PF 30-JUL-1997; 97US-0054212P.
 XX 30-JUL-1997; 97US-0054213P.
 XX 30-JUL-1997; 97US-0054214P.
 XX 30-JUL-1997; 97US-0054215P.
 XX 30-JUL-1997; 97US-0054217P.
 XX 30-JUL-1997; 97US-0054218P.
 XX 30-JUL-1997; 97US-0054234P.
 XX 30-JUL-1997; 97US-0054236P.
 XX 18-AUG-1997; 97US-0055968P.
 XX 18-AUG-1997; 97US-0055969P.
 XX 18-AUG-1997; 97US-0055972P.
 XX 19-AUG-1997; 97US-0056534P.
 XX 19-AUG-1997; 97US-0056543P.
 XX 19-AUG-1997; 97US-0056554P.
 XX 19-AUG-1997; 97US-0056561P.
 XX 19-AUG-1997; 97US-0056727P.
 XX 19-AUG-1997; 97US-0056729P.
 XX 19-AUG-1997; 97US-0056730P.
 XX 29-JUL-1998; 98WO-US015949.
 XX 26-JAN-1999; 99US-00236557.
 XX 21-SEP-2000; 2000US-00666984.
 XX 30-MAR-2001; 2001US-00820649.
 XX 05-JUN-2001; 2001US-0295558P.
 XX 04-JUN-2002; 2002US-00160162.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Feng P, Lafleur DM, Moore PA, Shi Y, Kyaw H, Li Y;
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
 XX WPI; 2005-161941/17.
 XX
 PT New nucleic acid molecule encoding human secreted protein, useful for
 PT preventing, treating, or ameliorating immune system, blood, inflammatory,
 PT infectious, cardiovascular, respiratory, neurological, endocrine, or
 XX reproductive disorders.
 XX
 PS Disclosure; SEQ ID NO 319; 309pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC human secreted proteins and peptides. The DNA and protein sequences of
 CC the invention are useful for treating or ameliorating: cancer, arthritis,
 CC asthma, AIDS, rheumatoid arthritis, inflammatory bowel disease, sepsis,
 CC acne, psoriasis, atherosclerosis, stroke, thrombosis, wound healing,
 CC Alzheimer's Disease, Parkinson's Disease, autism, obsessive compulsive
 CC disorder, graft-versus-host diseases, immune system disorders, blood
 CC disorders, inflammatory conditions, infectious diseases.
 CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
 CC respiratory disorders, neurological disorders, endocrine disorders, or
 CC reproductive disorders. The present sequence is that of a human peptide
 CC which is related to the novel human secreted proteins/peptides of the
 CC invention.
 XX
 SQ Sequence 14 AA;

Query Match 36.1%; Score 26; DB 9; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAKSV 9
 |||:|:
 Db 3 PFSISYSI 10

RESULT 56
 AEA36996

ID AEA36996 standard; peptide; 14 AA.
 XX
 AC AEA36996;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Novel laminin binding site antimicrobial peptide Seq121.
 XX
 KM antibacterial; fungicide; peptide therapy; bacterial infection;
 XX fungal infection.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 14
 FT /note="C-terminal amide"
 XX
 PN WO2005049819-A1.
 XX
 PD 02-JUN-2005.
 XX
 PF 25-OCT-2004; 2004WO-JP015803.
 XX
 PR 29-OCT-2003; 2003JP-00369595.
 XX
 PA (TOAG) TOA GOSEI KK.
 XX
 PI Yoshida T, Yamada Y, Kume M, Kourai H;
 XX WPI; 2005-396104/40.
 XX
 DR
 XX
 PT New artificially synthesized antimicrobial peptide capable of exerting an
 PT antimicrobial property with respect to bacteria or fungi, useful for
 PT treating bacterial infection and fungal infection.
 XX
 PS Claim 6; SEQ ID NO 21; 33pp; Japanese.
 XX
 CC This invention relates to a novel antimicrobial peptide capable of
 CC exerting an antimicrobial property with respect to bacteria or fungi. The
 CC peptide has a sequence comprising six consecutive amino acid residues
 CC chosen from an amino acid sequence comprising a laminin-binding site
 CC (UBS) or a sequence with amino acid substitutions in UBS, where the
 CC peptide does not exist naturally, and is thus artificially synthesized.
 CC The invention may be useful for the development of compounds with an
 CC antibacterial or fungicide activity via peptide therapy. The peptides
 CC effectively treat bacterial and fungal infections. The present sequence
 CC is that of a novel antimicrobial peptide of the invention. Note: The
 CC sequence listing does not form part of the written specification but was
 CC obtained by the indexer in electronic format directly from WIPO.
 XX
 SQ Sequence 14 AA;

Query Match 36.1%; Score 26; DB 9; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 KSVKSYLIG 15
 | | | | |
 Db 3 KKKRVLYLG 11

RESULT 57
 AEB18167
 ID AEB18167 standard; peptide; 14 AA.
 AC AEB18167;
 XX

DT 22-SEP-2005 (first entry)
 XX
 DE Prion disease-treatment peptide - SEQ ID 21.
 XX prion infection; cerebroprotective.
 XX

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OS Unidentified.
XX
XX JP2005192415-A.
XX
XX 21-JUL-2005.
XX
XX 26-DEC-2003; 2003JP-00435425.
XX
XX 26-DEC-2003; 2003JP-00435425.
XX
XX 26-DEC-2003; 2003JP-00435425.
XX
XX (TOAG ) TOA GOSEI CHEM IND LTD.
XX
XX Yoshida T;
XX
XX WPI; 2005-501994/51.
XX
XX
XX Novel non-natural peptide comprising amino acid residue of laminin
XX coupling region, nuclear localization signal (NLS) and BIPARTITE NLS,
XX useful for treating prion disease.
XX
XX
XX Claim 6; SEQ ID NO 21; 36pp; Japanese.
XX
XX
XX The invention comprises peptides which are useful for treating prion
XX disease, the peptides of the invention contain at least six continuous
XX amino acid residues of a laminin coupling/bond region. The peptides of
XX the invention are useful for treating prion disease. The present amino
XX acid sequence represents a prion disease treatment peptide of the
XX invention.
XX
XX Sequence 14 AA;
XX
XX
XX Query Match          36.1%; Score 26; DB 9; Length 14;
XX Best Local Similarity 66.7%; Pred. NO. 1.4e+03;
XX Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX
XX 7 KSVKSLYLIG 15
XX | | | | |
XX 3 KKRKVLYLIG 11
XX
XX
XX RESULT 58
XX ID AAM12084
XX AAM12084 standard; peptide; 15 AA.
XX
XX
XX AAM12084;
XX
XX 16-OCT-2003 (revised)
XX 02-APR-1997 (first entry)
XX
XX
XX T-cell epitope peptide 126 from HIV sf2 gp120.
XX
XX
XX T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
XX HIV sf2; herpes simplex virus; antigen gp2; tetanus toxoid; vaccine; HSV;
XX mammal; gp120; immune response; B-cell antigen.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9518148-A1.
XX
XX 06-JUL-1995.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX (CHIR-) CHIRON MINOTOPES PTY LTD.
XX
XX Geyzen HM, Rodda SJ;
XX
XX WPI; 1995-246333/32.
XX
XX T cell epitope peptide(s) - useful for detecting exposure of a subject to
XX an antigen or pathogen, and in vaccines for birds and mammals.
XX
XX

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```

XX
XX Example 3; Page 18; 57pp; English.
XX
XX
XX AAM12069-W12086 represent a pool of T-cell epitope peptides created from
XX HIV sf2 gp120 (see AAM11977). This pool of epitopes also contains the
XX sequences represented by AAM11953-W11960. T-cell epitopes (also known as
XX T-cell determinants) are peptides (or regions of a protein) which bind to
XX T-cell antigen receptors in conjugation with MHC proteins. AAM11953-
XX W11976 were the most antigenic peptides obtained from the pools of
XX peptides created from the HIV sf2 gp120 (see AAM11953-W11960), herpes
XX simplex virus antigen gp2 (see AAM11961-W11969), and tetanus toxoid (see
XX AAM11970-W11976). These sequences can be used in methods for detecting
XX exposure of a mammal or bird to an antigen, and for increasing the number
XX of T-cells specific for an antigen. The peptides can also be used in a
XX method for determining T-cell epitopes specific for an antigen. These
XX methods allow for the identification of T-cell determinants. The T-cell
XX epitope peptides can be used in a vaccine for inducing an immune response
XX in a bird or mammal. The vaccine also contains a B-cell antigen,
XX preferably herpes simplex virus gp2 (see AAM12068) or HIV sf2 gp120 (see
XX AAM11977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
XX field)
XX
XX
XX Sequence 15 AA;
XX
XX
XX Query Match          36.1%; Score 26; DB 2; Length 15;
XX Best Local Similarity 66.7%; Pred. NO. 1.6e+03;
XX Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 10 KSLYLIG 15
XX | | | | |
XX 8 KSIYIG 13
XX
XX
XX RESULT 59
XX ID AAM11956
XX AAM11956 standard; peptide; 15 AA.
XX
XX
XX AAM11956;
XX
XX 16-OCT-2003 (revised)
XX 02-APR-1997 (first entry)
XX
XX
XX T-cell epitope #4 from HIV sf2 gp120.
XX
XX
XX T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
XX HIV sf2; herpes simplex virus; antigen gp2; tetanus toxoid; vaccine; HSV;
XX mammal; gp120; immune response; B-cell antigen.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9518148-A1.
XX
XX 06-JUL-1995.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX (CHIR-) CHIRON MINOTOPES PTY LTD.
XX
XX Geyzen HM, Rodda SJ;
XX
XX WPI; 1995-246333/32.
XX
XX T cell epitope peptide(s) - useful for detecting exposure of a subject to
XX an antigen or pathogen, and in vaccines for birds and mammals.
XX
XX
XX Claim 1; Page 45; 57pp; English.
XX
XX AAM11953-W11976 represent T-cell epitope peptides. T-cell epitopes (also
XX known as T-cell determinants) are peptides (or regions of a protein)
XX which bind to T-cell antigen receptors in conjugation with MHC proteins.
XX These sequences were the most antigenic peptides obtained from pools of
XX

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CC peptides created from the HIV sf2 gp120 (AAW1953-W1960), herpes simplex
CC virus antigen gD2 (AAW1961-W1969), and tetanus toxoid (AAW1970-
CC W1976). These sequences can be used in methods for detecting exposure of
CC a mammal or bird to an antigen, and for increasing the number of T-cells
CC specific for an antigen. The peptides can also be used in a method for
CC determining T-cell epitopes specific for an antigen. These methods allow
CC for the identification of T-cell determinants. The T-cell epitope
CC peptides can be used in a vaccine for inducing an immune response in a
CC bird or mammal. The vaccine also contains a B-cell antigen, preferably
CC herpes simplex virus gD2 or HIV sf2 gp120 (see AAW1977), and a carrier.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 15 AA;
Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 10 KSLYLIG 15
DB 2 KSIYIG 7
RESULT 60
AAW12086
ID AAW12086 standard; peptide, 15 AA.
XX
XX AAW12086;
XX
XX 16-OCT-2003 (revised)
DT 02-APR-1997 (first entry)
XX
XX T-cell epitope peptide 128 from HIV sf2 gp120.
XX
XX T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KM HIV sf2; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV;
KM mammal; gp120; immune response; B-cell antigen.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9518148-A1.
XX
XX 06-JUL-1995.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
XX Geysen HM, Rodda SJ;
PI
XX
XX WPI; 1995-246333/32.
XX
XX T cell epitope peptide(s) - useful for detecting exposure of a subject to
XX an antigen or pathogen, and in vaccines for birds and mammals.
XX
XX Example 3; Page 18; 57pp; English.
XX
XX AAW12069-W12086 represent a pool of T-cell epitope peptides created from
CC HIV sf2 gp120 (see AAW1977). This pool of epitopes also contains the
CC sequences represented by AAW1953-W1960. T-cell epitopes (also known as
CC T-cell determinants) are peptides (or regions of a protein) which bind to
CC T-cell antigen receptors in conjugation with MHC proteins. AAW1953-
CC W1976 were the most antigenic peptides obtained from the pools of
CC peptides created from the HIV sf2 gp120 (see AAW1953-W1960), herpes
CC simplex virus antigen gD2 (see AAW1961-W1969), and tetanus toxoid (see
CC AAW1970-W1976). These sequences can be used in methods for detecting
CC exposure of a mammal or bird to an antigen, and for increasing the number
CC of T-cells specific for an antigen. The peptides can also be used in a
CC method for determining T-cell epitopes specific for an antigen. These
CC methods allow for the identification of T-cell determinants. The T-cell
CC epitope peptides can be used in a vaccine for inducing an immune response

CC in a bird or mammal. The vaccine also contains a B-cell antigen,
CC preferably herpes simplex virus gD2 (see AAW12068) or HIV sf2 gp120 (see
CC AAW1977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 15 AA;
Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 10 KSLYLIG 15
DB 4 KSIYIG 9
RESULT 61
AAW12085
ID AAW12085 standard; peptide, 15 AA.
XX
XX AAW12085;
XX
XX 16-OCT-2003 (revised)
DT 02-APR-1997 (first entry)
XX
XX T-cell epitope peptide 127 from HIV sf2 gp120.
XX
XX T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KM HIV sf2; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV;
KM mammal; gp120; immune response; B-cell antigen.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9518148-A1.
XX
XX 06-JUL-1995.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
XX Geysen HM, Rodda SJ;
PI
XX
XX WPI; 1995-246333/32.
XX
XX T cell epitope peptide(s) - useful for detecting exposure of a subject to
XX an antigen or pathogen, and in vaccines for birds and mammals.
XX
XX Example 3; Page 18; 57pp; English.
XX
XX AAW12069-W12086 represent a pool of T-cell epitope peptides created from
CC HIV sf2 gp120 (see AAW1977). This pool of epitopes also contains the
CC sequences represented by AAW1953-W1960. T-cell epitopes (also known as
CC T-cell determinants) are peptides (or regions of a protein) which bind to
CC T-cell antigen receptors in conjugation with MHC proteins. AAW1953-
CC W1976 were the most antigenic peptides obtained from the pools of
CC peptides created from the HIV sf2 gp120 (see AAW1953-W1960), herpes
CC simplex virus antigen gD2 (see AAW1961-W1969), and tetanus toxoid (see
CC AAW1970-W1976). These sequences can be used in methods for detecting
CC exposure of a mammal or bird to an antigen, and for increasing the number
CC of T-cells specific for an antigen. The peptides can also be used in a
CC method for determining T-cell epitopes specific for an antigen. These
CC methods allow for the identification of T-cell determinants. The T-cell
CC epitope peptides can be used in a vaccine for inducing an immune response
CC in a bird or mammal. The vaccine also contains a B-cell antigen,
CC preferably herpes simplex virus gD2 (see AAW12068) or HIV sf2 gp120 (see
CC AAW1977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 ||:|:|
 Db 6 KSIYIG 11

RESULT 62

AAW12083
 ID AAW12083 standard; peptide; 15 AA.

AC AAW12083;
 XX
 DT 16-OCT-2003 (revised)
 DT 02-APR-1997 (first entry)
 XX
 DE T-cell epitope peptide 125 from HIV sf2 gp120.

XX
 KM T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
 KM HIV sf2; herpes simplex virus; antigen gp2; tetanus toxoid; vaccine; HSV;
 KM mammal; gp120; immune response; B-cell antigen.

OS Human immunodeficiency virus 1.

PN MO9518148-A1.

XX 06-JUL-1995.

PD 28-DEC-1993; 93WO-US011703.

XX 28-DEC-1993; 93WO-US011703.

PR 28-DEC-1993; 93WO-US011703.

XX (CHIR-) CHIRON MIMOTOPES PTY LTD.

PI Geyesen HM, Rodda SJ;

XX WPI; 1995-246333/32.

XX T cell epitope peptide(s) - useful for detecting exposure of a subject to

PT an antigen or pathogen, and in vaccines for birds and mammals.

XX Example 3; Page 18; 57pp; English.

XX AAW12069-W12086 represent a pool of T-cell epitope peptides created from
 CC HIV sf2 gp120 (see AAW11977). This pool of epitopes also contains the
 CC sequences represented by AAW1953-W1960. T-cell epitopes (also known as
 CC T-cell determinants) are peptides (or regions of a protein) which bind to
 CC T-cell antigen receptors in conjugation with MHC proteins. AAW1953-
 CC W1976 were the most antigenic peptides obtained from the pools of
 CC peptides created from the HIV sf2 gp120 (see AAW1953-W1960), herpes
 CC simplex virus antigen gp2 (see AAW1961-W1969), and tetanus toxoid (see
 CC AAW1970-W1976). These sequences can be used in methods for detecting
 CC exposure of a mammal or bird to an antigen, and for increasing the number
 CC of T-cells specific for an antigen. The peptides can also be used in a
 CC method for determining T-cell epitopes specific for an antigen. These
 CC methods allow for the identification of T-cell determinants. The T-cell
 CC epitope peptides can be used in a vaccine for inducing an immune response
 CC in a bird or mammal. The vaccine also contains a B-cell antigen,
 CC preferably herpes simplex virus gp2 (see AAW12068) or HIV sf2 gp120 (see
 CC AAW1977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
 CC field)

XX Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 ||:|:|
 Db 10 KSIYIG 15

RESULT 63

AAW08008
 ID AAW08008 standard; peptide; 15 AA.

AC AAW08008;
 XX
 DT 16-OCT-2003 (revised)
 DT 03-FEB-1997 (first entry)
 XX
 DE V3 peptide #5.

XX HIV; gp120; HIV-IIIB strain; HIV-1 transmission; foetal transmission;
 KM neutralising antibody; passive immunisation; anti-idiotypic antibody;
 KM gp41; vaccine; active immunotherapy; V3.

OS Human immunodeficiency virus 1.

PN US556744-A.

XX 17-SEP-1996.

PF 24-MAR-1994; 94US-00218025.

XX 29-MAY-1992; 92US-00891451.

PR (UNIV-) UNIV PENNSYLVANIA.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Williams WV, Weiner DB, Ugen KE;

XX WPI; 1996-432980/43.

XX Determining the likelihood of maternal transmission of HIV-1 to foetus -
 PT by measuring maternal reactivity with specific gp120 and gp41 derived
 XX peptide(s), also used for diagnosing HIV in infants.

XX Disclosure; Col 109-110; 63pp; English.

XX AAW08004-W08015 represent HIV V3 peptides that can be used in the method
 CC of the invention. The method of the invention is for determining whether
 CC or not a mother will transmit HIV-1 to a foetus. The method comprises
 CC incubating a sample from the HIV-infected mother, with a collection of
 CC HIV peptides. The HIV peptides includes at least one gp41 derived peptide
 CC (see AAW07918-W07928), and at least one HIV gp120 derived peptide (see
 CC AAW07909-W07917). The number of peptides that react with the sample is
 CC determined, and this number is compared with a standard that shows
 CC pattern reactivity for a patient of transmission status. A non-
 CC transmissive HIV sample is indicated if the test sample reacts with twice
 CC as many peptides as the standard. The method detects the presence of
 CC neutralising antibodies that protect against mother to infant
 CC transmission of HIV. These sequences can also be used in vaccines to
 CC protect against transmission. Antibodies against these sequences can be
 CC used for passive immunisation, and to generate anti-idiotypic antibodies
 CC for use in vaccines or active immunotherapy. (Updated on 16-OCT-2003 to
 CC standardise OS field)

XX Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 ||:|:|
 Db 1 KSIYIG 6

RESULT 64

ABP30990
 ID ABP30990 standard; protein; 15 AA.

XX

AC ABP30990;
XX
DT 02-JUL-2002 (first entry)
XX
DE Peptide #40 that corresponds to 0772P specific antibody epitope.
XX
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
XX 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2002-164781/21.
XX
XX Poly peptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
XX Claim 33; Page 364; 408pp; English.
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.6e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PPSVAKSVKSLYL 14
|:|:|:|:|
Db 2 PYSLDKD--SLYL 12

RESULT 65
ABP56426
ID ABP56426 standard; peptide; 15 AA.
XX
AC ABP56426;
XX
DT 13-MAR-2003 (first entry)
XX
DE Human scorpion short chain toxic protein 18.59 peptide SEQ ID NO:7.
XX
KW Human; scorpion short chain toxic protein 18.59; malignant tumour;
KW haemopathy; human immunodeficiency virus infection; HIV infection;
KW immunological disease; inflammation.
XX
OS Homo sapiens.
XX
PN CN1352108-A.
XX
PD 05-JUN-2002.

XX
PF 06-NOV-2000; 2000CN-00127238.
XX
PR 06-NOV-2000; 2000CN-00127238.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-692404/75.
XX
PT New human scorpion short chain toxin protein 18.59 polypeptide for
PT treating malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX
CC The present invention describes human scorpion short chain toxin protein
CC 18.59 (I). Also described is a DNA recombination process used to produce
CC (I). (I) can be used for treating various diseases, such as malignant
CC tumours, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological diseases and various inflammations. The present sequence
CC represents the N-terminal peptide of (I), which is used in an example
CC from the present invention
XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPSVAKSVKSL 12
|:|:|:|:|
Db 3 PYQLKQKXAL 13

RESULT 66
ADA08653
ID ADA08653 standard; peptide; 15 AA.
XX
AC ADA08653;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human 0772P-specific antibody epitope #11.
XX
KW epitope; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX

SQ Sequence 15 AA;
Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 FSVAKSVKSLYL 14
DB 4 FSSQKGVKGLPL 15
RESULT 69
ADN94644
ID ADN94644 standard; peptide; 15 AA.
XX
AC ADN94644;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human 202P5A5v.1 protein epitope #4880.
XX
KM 202P5A5; human; cancer; tumour; epitope.
XX
OS Homo sapiens.
XX
FN WO2004016736-A2.
XX
PD 26-FEB-2004.
XX
PF 16-JUN-2003; 2003WO-US018906.
XX
PR 16-AUG-2002; 2002US-0404306P.
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Faris M, Challita-Eid PM, Jakobovits A, Ge W;
DR WPI; 2004-203774/19.
XX
PT New compositions having the 202P5A5 gene and encoded protein, useful for
PT diagnosing, preventing, prognosticating or treating cancer of the
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
PT bone and/or skin.
XX
PS Claim 1; Fig 2A; 266bp; English.
XX
CC The invention relates to a composition comprising 202P5A5 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 202P5A5v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ Sequence 15 AA;
Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 FSVAKSVKSLYL 14
DB 2 FSSQKGVKGLPL 13
RESULT 70
ADN94062
ID ADN94062 standard; peptide; 15 AA.
XX
AC ADN94062;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human 202P5A5v.1 protein epitope #4298.
XX

XX
KM 202P5A5; human; cancer; tumour; epitope.
XX
OS Homo sapiens.
XX
PN WO2004016736-A2.
XX
PD 26-FEB-2004.
XX
PF 16-JUN-2003; 2003WO-US018906.
XX
PR 16-AUG-2002; 2002US-0404306P.
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Faris M, Challita-Eid PM, Jakobovits A, Ge W;
DR WPI; 2004-203774/19.
XX
PT New compositions having the 202P5A5 gene and encoded protein, useful for
PT diagnosing, preventing, prognosticating or treating cancer of the
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
PT bone and/or skin.
XX
PS Claim 1; Fig 2A; 266bp; English.
XX
CC The invention relates to a composition comprising 202P5A5 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 202P5A5v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ Sequence 15 AA;
Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 FSVAKSVKSLYL 14
DB 4 FSSQKGVKGLPL 15
RESULT 71
ADN94078
ID ADN94078 standard; peptide; 15 AA.
XX
AC ADN94078;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human 202P5A5v.1 protein epitope #4314.
XX
KM 202P5A5; human; cancer; tumour; epitope.
XX
OS Homo sapiens.
XX
PN WO2004016736-A2.
XX
PD 26-FEB-2004.
XX
PF 16-JUN-2003; 2003WO-US018906.
XX
PR 16-AUG-2002; 2002US-0404306P.
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Faris M, Challita-Eid PM, Jakobovits A, Ge W;
DR WPI; 2004-203774/19.
XX

PT New compositions having the 202PSA5 gene and encoded protein, useful for
 PT diagnosing, preventing, prognosticating or treating cancer of the
 CC prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
 PT bone and/or skin.
 XX
 PS Claim 1; Fig 2A; 266pp; English.
 CC The invention relates to a composition comprising 202PSA5 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VIII-XXIX.
 XX
 SQ Sequence 15 AA;
 Query Match 36.1%; Score 26; DB 8; Length 15;
 Best Local Similarity 58.3%; Pred. No. 1.6e+03;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 FSVAKSVKSLYL 14
 Db 1 FSSQKGVKGLPL 12
 RESULT 72
 ADX17879
 ID ADX17879 standard; peptide; 15 AA.
 XX
 AC ADX17879;
 XX
 DT 21-APR-2005 (first entry)
 DE Human ovarian carcinoma antigen O772P antibody epitope #11.
 XX
 KM diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
 KM ovarian tumor; cancer; carcinoma; antigen.
 XX
 OS Homo sapiens.
 XX
 PN US2005031634-A1.
 XX
 PD 10-FEB-2005.
 XX
 PF 02-JUN-2004; 2004US-00860790.
 XX
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.
 PR 17-JUL-2002; 2002US-00198053.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Bangur CS, Rector MW, Fanger GR, Hill P;
 DR WPI; 2005-151645/16.
 XX
 PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
 PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
 PT for eliciting humoral and/or cellular immune response.
 XX
 PS Example 15; SEQ ID NO 500; 398pp; English.
 CC The invention relates to an isolated polynucleotide comprising a sequence
 CC of a sequence hybridizing under highly stringent conditions to, or
 CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
 CC the specification, its complement or degenerate variants, or a sequence
 CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The

CC polynucleotides and polypeptides are useful for diagnosing, preventing
 CC and treating diseases, such as ovarian cancer, and for eliciting humoral
 CC and/or cellular immune response. This sequence corresponds to an ovarian
 CC carcinoma antigen peptide of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 36.1%; Score 26; DB 9; Length 15;
 Best Local Similarity 53.8%; Pred. No. 1.6e+03;
 Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 QY 2 FSVAKSVKSLYL 14
 Db 2 PYSIDKD--SLYL 12
 RESULT 73
 ADM19018
 ID ADM19018 standard; peptide; 14 AA.
 XX
 AC ADM19018;
 XX
 DT 17-JUN-2004 (first entry)
 DE HLA-DR bound peptide SEQ ID NO:53.
 XX
 KM antigenic peptide; cytostatic; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; antibacterial; antidiabetic; antineumatic;
 KM antiarthritic; immunosuppressive; neuroprotective; dermatological;
 KM vaccine; T cell activator; cancer; melanoma; breast cancer;
 KM B cell lymphoma; prostate cancer; renal cancer; infectious disease; HIV;
 KM hepatitis C virus; measles virus; mycobacteria; autoimmune disease;
 KM rheumatoid arthritis; type I diabetes; multiple sclerosis;
 KM myasthenia gravis; systemic lupus erythematosus; HLA-DR bound peptide.
 XX
 OS Homo sapiens.
 XX
 PN EP1405862-A2.
 XX
 PD 07-APR-2004.
 XX
 PF 24-SEP-2003; 2003EP-00021521.
 XX
 PR 02-OCT-2002; 2002EP-00022223.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Kropshofer H, Vogt A;
 DR WPI; 2004-318705/30.
 XX
 PT Isolating antigenic peptides in femtomolar amounts, comprises providing
 PT complexes of peptide receptors with antigenic peptides isolated from
 PT mammalian organism, and eluting associated antigenic peptides from
 PT peptide receptors.
 XX
 PS Example 4; SEQ ID NO 53; 51pp; English.
 XX
 CC The present invention describes a method (M1) for isolating antigenic
 CC peptides (I) in femtomolar amounts, by providing complexes of peptide
 CC receptors with (I) isolated from mammal, and eluting associated (I) from
 CC peptide receptors, or providing complexes of peptide receptors with (I)
 CC isolated from cell or tissue of mammal, washing sequestered complexes of
 CC peptide receptors with (I), eluting associated (I) from peptide
 CC receptors, sequencing and identifying isolated peptides (II), which
 CC is a method for producing a pharmaceutical composition (III), which
 CC involves carrying out the steps of (M1), producing the identified
 CC peptides and optionally modifying them, and formulating the product
 CC obtained with a carrier or diluent (I) and (II) have cytostatic, anti-
 CC HIV, virucide, hepatotropic, antiinflammatory, antibacterial,
 CC antidiabetic, antineumatic, antiarthritic, immunosuppressive,
 CC neuroprotective and dermatological activities, and can be used in
 CC vaccines and as activators of T cells. (M1) is useful for isolating

CC antigenic peptides in femtomolar amounts, from a mammal such as human.
CC (M1) is useful for quality control of vaccines, immune monitoring of
CC diseases, control of the efficacy of a therapeutic treatment and design
CC of individualised peptide vaccines for the treatment of diseases. (M1) is
CC also useful for producing a pharmaceutical composition. The peptides
CC identified by (M1) are useful in vaccinating patients against cancer such
CC as melanoma, breast cancer, B cell lymphoma, prostate cancer and renal
CC cancer, infectious diseases such as diseases caused by HIV, hepatitis C
CC virus, measles virus and mycobacteria, and autoimmune diseases such as
CC rheumatoid arthritis, type I diabetes, multiple sclerosis, myasthenia
CC gravis and systemic lupus erythematosus. The present sequence represents
CC an HLA-DR bound peptide, which is used in an example from the present
CC invention.
XX
XX
SQ Sequence 14 AA;
XX
XX
Query Match 35.4%; Score 25.5; DB 8; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;
OY 4 SVAKSVKSL-YL 14
Db 2 AVVKSRIRIPYL 13
XX
XX
RESULT 74
ADM19019
XX ADM19019 standard; peptide; 15 AA.
XX
XX ADM19019;
XX
XX 17-JUN-2004 (first entry)
XX
XX HLA-DR bound peptide SEQ ID NO:54.
XX
XX
KM antigenic peptide; cytostatic; anti-HIV; virucide; hepatotropic;
KM antiinflammatory; antibacterial; antidiabetic; antirheumatic;
KM antiarthritic; immunosuppressive; neuroprotective; dermatological;
KM vaccine; T cell activator; cancer; melanoma; breast cancer;
KM B cell lymphoma; prostate cancer; renal cancer; infectious disease; HIV;
KM hepatitis C virus; measles virus; mycobacteria; autoimmune disease;
KM rheumatoid arthritis; type I diabetes; multiple sclerosis;
KM myasthenia gravis; systemic lupus erythematosus; HLA-DR bound peptide.
XX
XX
OS Homo sapiens.
XX
XX EPI405862-A2.
XX
XX PD 07-APR-2004.
XX
XX PF 24-SEP-2003; 2003EP-00021521.
XX
XX PR 02-OCT-2002; 2002EP-00022223.
XX
XX PA (HOF) HOFFMANN LA ROCHE & CO AG F.
XX
XX PI Kropshofer H, Vogt A;
XX
XX DR WPI; 2004-318705/30.
XX
XX PT Isolating antigenic peptides in femtomolar amounts, comprises providing
XX complexes of peptide receptors with antigenic peptides isolated from
XX mammalian organism, and eluting associated antigenic peptides from
XX peptide receptors.
XX
XX PS Example 4; SEQ ID NO 54; 51pp; English.
XX
XX CC The present invention describes a method (M1) for isolating antigenic
XX peptides (I) in femtomolar amounts, by providing complexes of peptide
XX receptors with (I) isolated from mammal, and eluting associated (I) from
XX peptide receptors, or providing complexes of peptide receptors with (I)
XX isolated from cell or tissue of mammal, washing sequestered complexes of
XX peptide receptors with (I), eluting associated (I) from peptide

CC receptors, sequencing and identifying isolated peptides. Also described
CC is a method for producing a pharmaceutical composition (II), which
CC involves carrying out the steps of (M1), producing the identified
CC peptides and optionally modifying them, and formulating the product
CC obtained with a carrier or diluent. (I) and (II) have cytostatic, anti-
CC HIV, virucide, hepatotropic, antiinflammatory, antibacterial,
CC antidiabetic, antirheumatic, antiarthritic, immunosuppressive,
CC neuroprotective and dermatological activities, and can be used in
CC vaccines and as activators of T cells. (M1) is useful for isolating
CC antigenic peptides in femtomolar amounts, from a mammal such as human.
CC (M1) is useful for quality control of vaccines, immune monitoring of
CC diseases, control of the efficacy of a therapeutic treatment and design
CC of individualised peptide vaccines for the treatment of diseases. (M1) is
CC also useful for producing a pharmaceutical composition. The peptides
CC identified by (M1) are useful in vaccinating patients against cancer such
CC as melanoma, breast cancer, B cell lymphoma, prostate cancer and renal
CC cancer, infectious diseases such as diseases caused by HIV, hepatitis C
CC virus, measles virus and mycobacteria, and autoimmune diseases such as
CC rheumatoid arthritis, type I diabetes, multiple sclerosis, myasthenia
CC gravis and systemic lupus erythematosus. The present sequence represents
CC an HLA-DR bound peptide, which is used in an example from the present
CC invention.
XX
XX
SQ Sequence 15 AA;
XX
XX
Query Match 35.4%; Score 25.5; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;
OY 4 SVAKSVKSL-YL 14
Db 3 AVVKSRIRIPYL 14
XX
XX
RESULT 75
AAI77393
XX AAI77393 standard; peptide; 8 AA.
XX
XX AC AAI77393;
XX
XX DT 22-MAY-2000 (first entry)
XX
XX DE HIV-1 group O env epitope, SEQ ID NO:109.
XX
XX KM HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
XX immunosassay; positive control; affinity purification; therapeutic;
XX Escherichia coli; reactive; epitope.
XX
XX OS Human immunodeficiency virus 1; group O.
XX
XX OS Synthetic.
XX
XX PN WO200004383-A2.
XX
XX PD 27-JAN-2000.
XX
XX PF 09-JUL-1999; 99WO-US015469.
XX
XX PR 14-JUL-1998; 98US-00115171.
XX
XX PA (ABBOTT) ABBOTT LAB.
XX
XX PI Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
XX
XX DR WPI; 2000-171290/15.
XX
XX PT Novel monoclonal antibodies useful as positive control reagent for
XX detecting human immunodeficiency virus infections and diagnosing,
XX evaluating or prognosing viral disease.
XX
XX PS Claim 18; Page 70; 148pp; English.
XX
XX CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which
XX may be used as positive control reagents in immunoassays to detect and

CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,
 CC which has no more than 15% cross reactivity to a corresponding antigen
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of
 CC using a monoclonal antibody as a positive control reagent in an
 CC immunoassay for the detection of anti HIV-1 group O antibodies. The
 CC monoclonal antibodies are useful as positive control reagents in
 CC immunoassays capable of detecting anti-HIV-1 Group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagents
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilised on a matrix and used
 CC for affinity purification of specific HIV-1 group O-derived proteins from
 CC cell cultures or biological tissues. The monoclonal antibodies can also
 CC be used for generating chimeric antibodies for therapeutic use. Different
 CC epitopes of HIV antigens can be used in combination in assay to diagnose,
 CC evaluate, or prognosticate HIV disease condition. The monoclonal
 CC antibodies are also useful for differentiating HIV-1 Group O antigens
 CC from HIV-group M and HIV-2 antigens. Sequences AAY77389-Y77398 represent
 CC HIV-1 group O env epitopes

XX SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 2,1e+06; Mismatches 0; Gaps 0;

OY 2 PFSVA 6
 |||||
 Db 1 PFSVA 5

RESULT 76

ABB76741
 ID ABB76741 standard; peptide; 8 AA.

XX ABB76741;

XX 31-MAY-2002 (first entry)

DE Tumour antigen epitope gp100209 presented by HLA A2.1.

XX Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;

KM human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.

XX Unidentified.

OS FR2812087-A1.

XX PD 25-JAN-2002.

XX PF 21-JUL-2000; 2000FR-00009591.

XX PR 21-JUL-2000; 2000FR-00009591.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;

XX DR WPI; 2002-189846/25.

XX PT Identifying subdominant or cryptic epitopes, useful in immunotherapy of
 PT cancer and viral infection, comprises testing modified, non-immunogenic
 PT peptides for induction of cytotoxic T cells.

XX PS Example 1; Page 12; 62pp; French.

XX CC The present invention relates to subdominant/cryptic epitopes that are
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
 CC epitopes or chimeric polypeptides containing them and nucleic acid
 CC encoding them are useful for preventative or curative immunotherapy of

CC cancer and viral infections, particularly where used as vaccines. The
 CC present peptide was used to illustrate the invention

XX SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 5; Length 8;

Best Local Similarity 100.0%; Pred. No. 2,1e+06; Mismatches 0; Gaps 0;

OY 1 VPFSV 5
 |||||
 Db 4 VPFSV 8

RESULT 77

ADH62104
 ID ADH62104 standard; peptide; 8 AA.

XX ADH62104;

XX 25-MAR-2004 (first entry)

DE Cyclic antiviral peptide, SEQ ID NO:83.

KM Antiviral peptide; prophylaxis; therapy; drug screening; virucide;
 KM hepatotropic; antiinflammatory; vaccine; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 2 /note= "D-form residue"

FT MISC-difference 4 /note= "D-form residue"

FT MISC-difference 6 /note= "D-form residue"

FT MISC-difference 8 /note= "D-form residue"

XX W02003092631-A2.

XX PD 13-NOV-2003.

XX PF 06-MAY-2003; 2003WO-US014372.

XX PR 06-MAY-2002; 2002US-0378256P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Ghadiri MR;

XX DR WPI; 2004-042365/04.

XX PT New fast-acting cyclic peptide anti-viral agents that do not cause
 PT undesired lysis of animal cells, useful for the preparation of a
 PT medicament for the prevention and/or treatment of viral infections.
 XX PS Example 2; SEQ ID NO 83; 239pp; English.

XX CC The invention relates to cyclic antiviral peptides which do not cause
 CC undesired lysis of animal cells. The cyclic peptides are composed of 4-16
 CC alternating L- and D-form amino acids. The invention also relates to use
 CC of the cyclic peptides for treating and preventing viral infection,
 CC particularly adenoviral infection, in an animal; pharmaceutical
 CC compositions comprising a peptide of the invention; and methods for
 CC identifying or evaluating a cyclic peptide with anti-viral activity. The
 CC peptides are substantially non-toxic to mammals and may be used to treat
 CC or prevent infection by a wide variety of viruses. These viruses include:
 CC hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus
 CC (HCV), human immunodeficiency virus (HIV), herpes virus, adenovirus,
 CC parvovirus, parvovirus, reovirus, orbivirus, picornavirus, rotavirus,
 CC alphavirus, rubivirus, influenza virus (type A and type B), flavivirus,
 CC coronavirus, paramyxovirus, morbillivirus, pneumovirus, rhabdovirus,

CC lyssavirus, orthomyxovirus, bunyavirus, phlebovirus, nairovirus,
CC hepdnavirus, arenavirus, retrovirus, rhinovirus, filovirus,
CC haemorrhagic fever virus, Chikungunya virus, Japanese encephalitis virus,
CC monkey pox virus, varicella virus, Congo-Crimean haemorrhagic fever virus,
CC Junin virus, Onk haemorrhagic fever virus, Venezuelan equine
CC encephalitis virus, Dengue fever virus, Lassa fever virus, Rift valley
CC fever virus, western equine encephalitis virus, eastern equine
CC encephalitis virus, lymphocytic choriomeningitis virus, Russian spring-
CC summer encephalitis virus, white pox virus, Ebola virus, Machupo virus,
CC smallpox virus, yellow fever virus, Hantaan virus, Marburg virus or tick-
CC borne encephalitis virus. The present sequence represents a cyclic
CC antiviral peptide used in an example of the invention.
XX
SQ Sequence 8 AA;
XX
Query Match 34.7%; Score 25; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 7 KSVKSLYL 14
DB 1 KSKKLYL 8
XX
RESULT 78
ADP67919
ID ADP67919 standard; peptide; 8 AA.
XX
AC ADP67919;
XX
DT 12-AUG-2004 (first entry)
XX
DE Anti-microbial cyclic peptide #83.
XX
KW microbial infection; cyclic; circular; anthrax infection;
KW staph infection; typhus; food poisoning; bacillary dysentery; pneumonia;
KW cholera; ulcer; botulism; smallpox; listeriosis; tularemia; plague;
KW bubonic plague; pneumonic plague; diarrhoea; hemorrhagic colitis;
KW haemolytic uremic syndrome; thrombotic thrombocytopenic purpura;
KW rabbit fever; deerfly fever; O'hara's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 6 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
XX
PN WO2003093300-A2.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-US014240.
XX
PR 06-MAY-2002; 2002WO-US014329.
XX
PI (SCRI) SCRIPPS RES INST.
XX
PI Ghadiri MR, Kim HS, Fernandez-Lopez S, Wilcoxen K;
XX
DR WPI; 2004-169024/16.
XX
PT Composition useful for the treatment of microbial infections e.g. anthrax
PT infection, staph infection comprises a cyclic peptide.
XX
PS Example 2; SEQ ID NO 83; 247pp; English.
XX
CC The invention comprises a composition for treating or preventing

CC microbial infection in an animal. The composition of the invention
CC contains a carrier and a cyclic peptide having a sequence of about 4-16
CC alternating D- and L-alpha-amino acids. The composition of the invention
CC is useful for the treatment of microbial infection, such as: anthrax
CC infection, staph infection, typhus, food poisoning, bacillary dysentery,
CC pneumonia, cholera, ulcers, botulism, smallpox, listeriosis, tularemia,
CC plague, bubonic plague, pneumonic plague, diarrhoea, hemorrhagic colitis,
CC haemolytic uremic syndrome, thrombotic thrombocytopenic purpura, rabbit
CC fever, deerfly fever and O'hara's disease. The present amino acid
CC sequence represents an anti-microbial cyclic peptide of the invention.
XX
SQ Sequence 8 AA;
XX
Query Match 34.7%; Score 25; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 7 KSVKSLYL 14
DB 1 KSKKLYL 8
XX
RESULT 79
ADQ28132
ID ADQ28132 standard; peptide; 8 AA.
XX
AC ADQ28132;
XX
DT 09-SEP-2004 (first entry)
XX
DE Excluded cyclic antifungal peptide therapeutic agent #89.
XX
KW cyclic; fungicide; dermatological; antifungal; respiratory;
KW gastrointestinal; cardiovascular; uropathic; central nervous system;
KW auditory; fungal cell death inducer; medicament; fungal infection; human;
KW farm animal; systemic infection; topical infection;
KW dermatophytic fungal infection; onychomycosis; Epidermophyton;
KW Microsporium; Trichophyton rubrum; allergy; respiratory tract infection;
KW mucosal membrane infection; gastrointestinal tract infection;
KW cardiovascular infection; urinary tract infection; candidiasis;
KW mucocandidiasis; ringworm; tinea infection; athlete's foot; paronychia;
KW pityriasis versicolor; erythrasma; intertrigo; fungal nappy rash;
KW candida vulvitis; candida balanitis; otitis externa; cancer therapy;
transplant patient.
XX
OS Synthetic.
XX
PN WO2004050685-A2.
XX
PD 17-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038595.
XX
PR 29-NOV-2002; 2002US-0429923P.
XX
PI (ADAP-) ADAPTIVE THERAPEUTICS INC.
XX
PI (WEIN/) WEINBERGER D.
XX
PI (SANC/) SANCHEZ-QUESADA J.
XX
PI (CABE/) CABEZAS E.
XX
PI Sanchez-Quesada J, Cabezas E;
XX
DR WPI; 2004-487528/46.
XX
PT New peptide comprising a cyclic amino acid sequence of four to ten
PT alternating D- and L-alpha amino acids useful for treating fungal
PT infections.
XX
PS Claim 20; Page 66; 76pp; English.
XX
CC The invention relates to a peptide comprising a cyclic amino acid
CC sequence of 4-10 (preferably 6 or 8) alternating D- and L-alpha amino
CC acids (preferably polar, nonpolar and ionizable). The peptide is useful

CC in the manufacture of a medicament for treating or preventing fungal
 CC infection in an animal e.g. human, farm animal or companion animal
 CC including systemic, topical, dermatophytic fungal infection; for treating
 CC onychomycosis caused by Epidermophyton, Microsporum and Trichophyton
 CC rubrum; for treating allergy, respiratory tract infection, mucosal
 CC membrane infection, gastrointestinal tract infection, cardiovascular
 CC infection, urinary tract infection, CNS infection, candidiasis and
 CC chronic mucocandidiasis and skin infections caused by fungi, ringworm and
 CC trinea infections, athlete's foot, paronychia, pityriasis versicolor,
 CC erythrasma, intertrigo, fungal nappy rash, candida vulvitis, candida
 CC balanitis and ocular externa and infections in immunocompromised patients
 CC (e.g. AIDS patients, patients receiving cancer therapy or transplant
 CC patients). The peptides possess antifungal activity without undesired
 CC anti-animal cell activity; have a minimum inhibitory concentration at
 CC which no target fungal organism grow in vitro is less than one twentieth
 CC to less than half of the peptide concentration needed to cause 50%
 CC hemolysis of mammalian red blood cells in vitro ; causes no hemolysis of
 CC mammalian red blood cells in vitro ; are proteolytically stable and easy
 CC to synthesize and are highly effective against broad range of fungal
 CC infections. Sequences ADQ28003 to ADQ28043 correspond to claimed examples
 CC of the peptide of the invention. Specifically excluded as peptides of the
 CC invention are the sequences ADQ28044 to ADQ28180.

XX SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 8; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.1e+06; Mismatches 0; Gaps 0;

Matches 6; Conservative 0; Indels 2;

QY 7 KSVKSLYL 14
 || || || ||
 Db 1 KSSKYL 8

RESULT 80

ID AAR84828 standard; peptide; 9 AA.

XX AAR84828;

AC 25-APR-1996 (first entry)

XX Modified melanocyte-melanoma specific antigenic peptide G9-209-213W.

XX MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;

KM metastatic melanoma; tumour-associated antigen; immunogenic peptide;

KW diagnosis; prognosis; prophylaxis; therapy; vaccine.

XX Synthetic.

OS W09529193-A2.

XX 02-NOV-1995.

XX 21-APR-1995; 95MO-US005063.

XX 22-APR-1994; 94US-00231565.

PR 05-APR-1995; 95US-00417174.

XX (USSH) US SEC DEPT HEALTH.

XX Kawakami Y, Rosenberg SA;

PI WPI; 1995-382963/49.

XX DNA encoding melanoma antigens recognised by T-lymphocytes - also

PT vectors, host cells and antibodies, used to detect, treat and immunise

XX animal against melanoma.

XX Example 5; Page 107; 184pp; English.

XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-

CC 209 is an immunogenic peptide based on the melanoma derived antigen,

CC gp100 (see AAR84210). The peptides are used in medicaments for the
 CC treatment or prevention (by immunization) of melanoma. Antibodies against
 CC MART-1 and its immunogenic peptides may be used in the detection and
 CC isolation of MART-1 from a sample, the detection of which is indicative
 CC of a disease state (melanoma or metastatic melanoma)

XX SQ Sequence 9 AA;

Query Match 34.7%; Score 25; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Mismatches 0; Gaps 0;

Matches 5; Conservative 0; Indels 0;

QY 1 VPFSV 5
 |||||
 Db 5 VPFSV 9

Search completed: July 12, 2006, 05:34:18
 Job time : 218 secs

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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:34:39 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-671-019-2
Perfect score: 72
Sequence: 1 VPFSVAKSVKSLYIG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 800 summaries

Database : PIR 80: *
1: pirl: *
2: pirl: *
3: pirl: *
4: pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	34.7	14	2 PH0774	T-cell receptor be
2	25	34.7	14	2 CS9137	protein PFI - gold
3	24	33.3	15	2 S49409	H+-transporting tw
4	23	31.9	10	2 A44871	monodehydroascorba
5	23	31.9	13	2 S47372	T-cell antigen rec
6	23	31.9	14	2 JN0390	histamine-releasin
7	23	31.9	14	2 G61308	hemocyanin chain 3
8	22	30.6	13	2 S47365	T-cell antigen rec
9	22	30.6	15	2 S43634	cytochrome-c oxida
10	20	27.8	12	2 E45691	probable minor cap
11	20	27.8	13	2 S47360	T-cell antigen rec
12	20	27.8	12	2 S47374	T-cell antigen rec
13	20	27.8	13	4 I70075	glycophorin B (mis
14	20	27.8	13	2 A61362	bradykinin-like pe
15	19	26.4	10	2 S68033	cytochrome P450 1A
16	19	26.4	11	2 B43669	hypothetical prote
17	19	26.4	12	2 S26582	T-cell receptor be
18	19	26.4	12	2 S26549	T-cell receptor be
19	19	26.4	12	2 S26553	T-cell receptor be
20	19	26.4	12	2 PH1469	T-cell receptor be
21	19	26.4	14	2 S09721	2S albumin small c
22	19	26.4	14	2 A44920	2-halobenzamide 1,2
23	18	25.0	7	2 JN0859	peptidyl-dipeptida
24	18	25.0	10	2 A60624	angiotensin I - ja
25	18	25.0	10	2 A90917	angiotensin precur
26	18	25.0	11	2 PH1375	T antigen variant
27	18	25.0	12	2 S21163	NMD ADF-ribosyltra
28	18	25.0	12	2 PH1463	T-cell receptor be
29	18	25.0	12	2 PH1464	T-cell receptor be

30	18	25.0	12	2 PH1468	T-cell receptor be
31	18	25.0	12	2 C60529	hemocyanin 1 - gre
32	18	25.0	13	2 S47384	T-cell antigen rec
33	18	25.0	13	2 B61620	locustaminotropin I
34	18	25.0	14	1 NYP614	hypothalamic tetra
35	18	25.0	15	2 B59137	protein PFI - gold
36	17	23.6	7	2 PC2132	FMRFamide-related
37	17	23.6	10	2 A13687	caerulein-like pep
38	17	23.6	10	2 C39745	sphingomyelinase -
39	17	23.6	11	2 B49164	chromogranin-B - r
40	17	23.6	11	2 PC2372	58K heat shock pro
41	17	23.6	12	2 S43957	Ig mu chain V regi
42	17	23.6	12	2 PH0785	T-cell receptor al
43	17	23.6	12	2 P00696	1,4-alpha-glucan b
44	17	23.6	13	2 PT0263	Ig heavy chain CRD
45	17	23.6	13	2 S47356	T-cell antigen rec
46	17	23.6	13	2 S47359	T-cell antigen rec
47	17	23.6	13	2 S47371	T-cell antigen rec
48	17	23.6	13	2 S47373	T-cell antigen rec
49	17	23.6	13	2 S47380	T-cell antigen rec
50	17	23.6	13	2 S47390	T-cell antigen rec
51	17	23.6	13	2 S47382	T-cell antigen rec
52	17	23.6	13	2 S20578	ribosomal protein
53	17	23.6	13	2 JZVHP1	crabrolin - Europe
54	17	23.6	14	1 QMVPB2	mastoparan C - Eur
55	17	23.6	14	2 PA0015	seed storage prote
56	17	23.6	14	2 PT0223	Ig heavy chain CDR
57	17	23.6	14	2 S36678	dodecenoyl-CoA Del
58	17	23.6	15	1 LFECF	pne operon leader
59	17	23.6	15	2 PH0784	T-cell receptor al
60	17	23.6	15	2 PH0797	T-cell receptor al
61	17	23.6	15	2 PH0750	T-cell receptor be
62	17	23.6	15	2 PH0751	T-cell receptor be
63	17	23.6	15	2 S77987	cytochrome-c oxida
64	17	23.6	15	2 A41436	alpha-macroglobuli
65	16	22.2	6	2 A61140	sperm acrosomal pr
66	16	22.2	9	2 C24180	fibrinogen beta ch
67	16	22.2	9	2 PC7073	ubiquitinol-cytochro
68	16	22.2	10	2 PC4442	cytochrome c553 -
69	16	22.2	11	2 PU0029	33K protein 3218 -
70	16	22.2	11	2 S58244	pyrroloquinoline q
71	16	22.2	11	2 H84082	hypothetical prote
72	16	22.2	11	2 S00616	parasporal crystal
73	16	22.2	12	1 LFECPE	pyre leader peptid
74	16	22.2	12	2 A28856	fructose-bisphosph
75	16	22.2	13	2 S47362	T-cell antigen rec
76	16	22.2	13	2 S47368	T-cell antigen rec
77	16	22.2	13	2 S47400	T-cell antigen rec
78	16	22.2	13	2 A60336	outer membrane pro
79	16	22.2	14	2 S13864	methyl coenzyme M
80	16	22.2	14	2 S11074	alcohol dehydrogen
81	16	22.2	14	2 G33160	H+-transporting tw
82	16	22.2	15	2 PH0752	T-cell receptor be
83	16	22.2	15	2 PH0117	hemoglobin alpha c
84	15	20.8	7	2 S71870	glutathione transf
85	15	20.8	8	2 P00012	cholecystokinin -
86	15	20.8	9	2 A43001	cholecystokinin -
87	15	20.8	9	2 I52974	seminal vesicle pr
88	15	20.8	9	2 S66635	alpha-2-macroglobu
89	15	20.8	10	2 S63478	dihydroallopinamide d
90	15	20.8	10	2 S65728	hemoglobin, extrac
91	15	20.8	10	2 D37397	hypothetical prote
92	15	20.8	10	2 A39745	endo-glucosylceram
93	15	20.8	11	1 EOCC	eledostin - musky
94	15	20.8	11	1 EOCC	eledostin - curied
95	15	20.8	11	2 PD0441	translation elongac
96	15	20.8	11	2 PH0941	T-cell receptor be
97	15	20.8	11	2 A61365	phyllotoxinin - Rohd
98	15	20.8	12	2 S47363	T-cell antigen rec
99	15	20.8	12	2 S69095	ubiquitinol-cytochro
100	15	20.8	12	2 PH1454	T-cell receptor al
101	15	20.8	12	2 A61360	vespakinin M - hor
102	15	20.8	12	2 A61359	vespakinin X - hor

103	15	20.8	13	2	S47382	T-cell antigen rec
104	15	20.8	13	2	S47389	T-cell antigen rec
105	15	20.8	13	2	PH0787	T-cell receptor al
106	15	20.8	13	2	PC1008	40K extracellular
107	15	20.8	13	2	S78766	ribosomal protein
108	15	20.8	13	2	S74130	NADH oxidase - Gla
109	15	20.8	14	2	A47421	leukotriene B-4 12
110	15	20.8	14	2	JN0389	histamine-releasin
111	15	20.8	14	2	PH1705	Ig heavy chain V r
112	15	20.8	14	2	B34135	DNA-binding protei
113	15	20.8	14	2	PH1566	cerebrin 30 huma
114	15	20.8	14	2	A28018	very late antigen-
115	15	20.8	14	2	D35141	T-cell receptor de
116	15	20.8	14	2	C35141	T-cell receptor de
117	15	20.8	14	2	E35141	T-cell receptor de
118	15	20.8	14	2	B44854	L-2, 4-diaminobuty
119	15	20.8	15	2	S61284	phosphoprotein, 80
120	15	20.8	15	2	PS0452	32K protein 3306 -
121	15	20.8	15	2	PA0057	adenylate isopente
122	15	20.8	15	2	PS0221	gasstrin-releasing
123	15	20.8	15	2	S47387	T-cell antigen rec
124	15	20.8	15	2	PH1590	Ig H chain V-D-J r
125	15	20.8	15	2	B35141	T-cell receptor de
126	15	20.8	15	2	A35141	NADH2 dehydrogena
127	15	20.8	15	2	PQ0781	ribosomal protein
128	15	20.8	15	2	S36896	protein QP20006 -
129	15	20.8	15	2	PA0053	beaded-chain beta ch
130	15	20.8	15	2	A32921	hemoglobin beta ch
131	15	20.8	15	2	PN0118	ubiquitin-carrier
132	15	20.8	15	2	A54397	entactin/nidogen -
133	15	20.1	12	2	A54315	translatin elonga
134	14.5	20.1	15	2	PA0110	ubiquitin - celerly
135	14	19.4	8	2	A61496	psa protein - Erw
136	14	19.4	8	2	S37141	neuropeptide calla
137	14	19.4	8	2	D47393	endospem protein,
138	14	19.4	9	2	S70334	cardioactive pepit
139	14	19.4	9	2	S39766	Ig heavy chain CRD
140	14	19.4	9	2	PT0285	cytochrome-c oxida
141	14	19.4	9	2	S77984	hypothetical E2 pr
142	14	19.4	9	4	I73804	mannose receptor -
143	14	19.4	10	2	S39374	Ig H chain V-D-J r
144	14	19.4	10	2	PH1633	hypothetical prote
145	14	19.4	10	2	S06964	formaldehyde dehyd
146	14	19.4	10	2	D46285	sperm-activating p
147	14	19.4	10	2	G60787	Ig heavy chain CRD
148	14	19.4	10	2	E60787	hypothetical E2 pr
149	14	19.4	11	2	PT0250	mannose receptor -
150	14	19.4	11	2	PD0442	Ig heavy chain CRD
151	14	19.4	11	2	S60294	NIPENAR2 protein -
152	14	19.4	11	2	S78765	tubulin 2 beta-3 c
153	14	19.4	11	2	B26744	ribosomal protein
154	14	19.4	11	2	S17869	megascorliakinin -
155	14	19.4	12	2	PD0021	glutathione transf
156	14	19.4	12	2	S10624	muconate cyclisom
157	14	19.4	12	2	S65136	lipovitellin - Afr
158	14	19.4	12	2	S57570	kallikrein K2 - hu
159	14	19.4	12	2	PH0930	T cell receptor V-
160	14	19.4	12	2	PH1470	T-cell receptor be
161	14	19.4	12	2	S29859	T-cell receptor de
162	14	19.4	12	2	PD0730	gene p10 protein -
163	14	19.4	12	2	A54326	undentified 5.4/3
164	14	19.4	12	2	A56878	light yellow cell
165	14	19.4	12	2	I77529	estrogen receptor
166	14	19.4	12	2	S36887	NADH2 dehydrogena
167	14	19.4	13	2	PS0325	ribosomal protein
168	14	19.4	13	2	A54326	tetrahydroberberin
169	14	19.4	13	2	PT0290	glutathione transf
170	14	19.4	13	2	S47377	glandular kallikre
171	14	19.4	13	2	S47381	Ig heavy chain CRD
172	14	19.4	13	2	S47385	T-cell antigen rec
173	14	19.4	13	2	B36042	T-cell antigen rec
174	14	19.4	13	2	PN0168	oxix protein - Bac
175	14	19.4	14	1	QWVHM	phosphopyruvate hy
						mascoparan W - hor

176	14	19.4	14	1	QWVHXX	mascoparan X - hor
177	14	19.4	14	1	QWAVV	mascoparan - yello
178	14	19.4	14	2	S19803	ubiquitin - potaro
179	14	19.4	14	2	I51432	histone H4-1 precu
180	14	19.4	14	2	PT0077	proteochondotin c
181	14	19.4	14	2	E61308	hemocyanin chain 3
182	14	19.4	14	2	B20872	alpha-2-macroglobu
183	14	19.4	14	2	S57574	T cell receptor V-
184	14	19.4	14	2	PH0804	T-cell receptor al
185	14	19.4	14	2	A54370	inorganic diphosph
186	14	19.4	14	2	S58862	botulinum neurotox
187	14	19.4	14	2	PQ0058	glycerol kinase (E
188	14	19.4	14	2	S33802	chaperone, TCPI-re
189	14	19.4	14	2	S14336	mascoparan B - hor
190	14	19.4	14	2	PL0040	glycogen phosphory
191	14	19.4	14	2	PC7075	guanylate cyclase
192	14	19.4	14	2	E81280	probable proteolys
193	14	19.4	14	2	PA0040	malate dehydrogena
194	14	19.4	14	2	PS0276	phosphoribulokinas
195	14	19.4	14	2	E41383	23K variable histo
196	14	19.4	14	2	PA0026	protein QA300027 -
197	14	19.4	14	2	PS0218	24K protein 4413 -
198	14	19.4	14	2	B61457	alpha-glucosidase
199	14	19.4	14	2	S57577	T cell receptor V-
200	14	19.4	14	2	D46743	corneal keratan su
201	14	19.4	14	2	S21293	RIP protein - rat
202	14	19.4	14	2	PL0110	complement factor
203	14	19.4	14	2	PT0095	H+-transporting tw
204	14	19.4	14	2	PH1449	T-cell receptor al
205	14	19.4	14	2	E91061	hypothetical prote
206	14	19.4	14	2	S71920	proteinase ECP 32
207	14	19.4	14	2	S36891	ribosomal protein
208	14	19.4	14	2	S20410	protein kinase (EC
209	14	19.4	14	2	PA0091	methionine adenosy
210	14	19.4	14	2	PA0063	ubiquitin - fungus
211	14	19.4	14	2	A60221	apolipoprotein A-I
212	14	19.4	14	2	A61522	7.5K surfactant-as
213	14	19.4	14	2	A32971	heparin-binding le
214	14	19.4	14	2	S03955	acidic fibroblast
215	14	19.4	14	2	PU0025	ubiquitin-cytochro
216	14	19.4	14	2	I40665	IL18N leader pepit
217	13	18.1	13	2	PT0278	Ig heavy chain CRD
218	13	18.1	13	2	PT0597	T-cell receptor be
219	13	18.1	13	2	JS0319	subesophageal gang
220	13	18.1	13	2	A61049	halo-toxin - Pseud
221	13	18.1	13	2	I51317	bHNF transcription
222	13	18.1	13	2	PQ0663	membrane protein -
223	13	18.1	13	2	PS0254	18K protein 5507 -
224	13	18.1	13	2	E33932	Ig mu chain D regi
225	13	18.1	13	2	A28340	myomodulin - Calif
226	13	18.1	13	2	A42057	fibroblast growth
227	13	18.1	13	2	A61467	penalbumin - Adeli
228	13	18.1	13	2	I48934	apolipoprotein A-I
229	13	18.1	13	2	TI3818	cytochrome oxidase
230	13	18.1	13	2	YEPG	thymic factor - pi
231	13	18.1	13	2	A60957	endospem protein,
232	13	18.1	13	2	S70332	bradykinin - horn
233	13	18.1	13	2	S65433	cardioactive pepit
234	13	18.1	13	2	S39767	cardioactive pepit
235	13	18.1	13	2	A26363	locustamytotropin I
236	13	18.1	13	2	A61620	cardioactive pepit
237	13	18.1	13	2	S27233	serum amyloid P-co
238	13	18.1	13	2	B20569	cytokeratin 4 - bo
239	13	18.1	13	2	I46016	bone gla protein -
240	13	18.1	13	2	I49406	hydroxyproline-3-b
241	13	18.1	13	2	A43065	pev-tachykinin - p
242	13	18.1	13	2	PD0027	vitamin D3 26-mono
243	13	18.1	13	2	S15850	bradykinin-like pe
244	13	18.1	13	2	A26744	Thr-6 bradykinin -
245	13	18.1	13	2	A61057	bradykinin-like pe
246	13	18.1	13	2	A60579	bradykinin - commo
247	13	18.1	13	2	A61363	bradykinin-like pe
248	13	18.1	13	2	A61358	bradykinin-like pe

249	13	18.1	13	2	A61358	bradykinin-like pe
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249	13	18.1	10	2	PA0050	protein QA100052 -	322	13	18.1	14	2	PH1763	T cell receptor a1
250	13	18.1	10	2	PS0209	24K protein 4407 -	323	13	18.1	14	2	S57569	T cell receptor V-
251	13	18.1	10	2	S65432	angiotensin I - ho	324	13	18.1	14	2	S57538	T cell receptor V-
252	13	18.1	10	2	A32195	Na+/K+-exchanging	325	13	18.1	14	2	PH1598	Ig H chain V-D-J r
253	13	18.1	10	2	A27617	cytochrome-phosphate i	326	13	18.1	14	2	PH0765	T-cell receptor be
254	13	18.1	10	2	S77980	cytochrome-c oxida	327	13	18.1	14	2	PH0755	T-cell receptor be
255	13	18.1	10	2	A90345	angiotensin precu	328	13	18.1	14	2	PH1471	T-cell receptor be
256	13	18.1	10	2	C54226	light-harvesting p	329	13	18.1	14	2	B61597	cytochrome P450 AL
257	13	18.1	10	2	PO0788	NMDH2 dehydrogenas	330	13	18.1	14	2	S21747	glutamate dehydrog
258	13	18.1	10	2	C60527	sperm-activating p	331	13	18.1	15	2	S24159	leukocyte elastase
259	13	18.1	11	2	A38841	rhodopsin homolog	332	13	18.1	15	2	A60834	angiotensin I prec
260	13	18.1	11	2	I54193	Rhesus blood group	333	13	18.1	15	2	I58116	Dp116 - human
261	13	18.1	11	2	PA0028	protein QA300042 -	334	13	18.1	15	2	S65717	prostaglandin D-sy
262	13	18.1	11	2	G61497	seed protein ws-23	335	13	18.1	15	2	PM0004	nitrogenase cofact
263	13	18.1	11	2	F33098	214K exantigen (v	336	13	18.1	15	2	S32577	hypothetical 1.7K
264	13	18.1	11	2	A54348	N-acetylglycosamin	337	13	18.1	15	2	UN0730	hypothetical 1.7K
265	13	18.1	11	2	PH1376	T antigen variant	338	13	18.1	15	2	PA0001	photosystem I iron
266	13	18.1	11	2	PH0938	T-cell receptor be	339	13	18.1	15	2	PA0024	photosystem I, iro
267	13	18.1	11	2	F58501	43.5K bile stone p	340	13	18.1	15	2	PA0114	photosystem I, iro
268	13	18.1	11	2	S66506	quinoline 2-oxidor	341	13	18.1	15	2	PA0080	translation elonga
269	13	18.1	11	2	S04875	nifs protein - Bra	342	13	18.1	15	2	S71300	ICL3 protein - Par
270	13	18.1	11	2	S69349	neuropeptide Frami	343	13	18.1	15	2	C61511	milk band B protei
271	13	18.1	11	2	S13279	lie-ser-bradykinin	344	13	18.1	15	2	PH1365	Ig heavy chain DJ
272	13	18.1	11	2	A59146	conotoxin a5a - c	345	13	18.1	15	2	S05700	insulin-like growt
273	13	18.1	11	2	S07207	Crina-angiotensin	346	13	18.1	15	2	D28587	T-cell receptor be
274	13	18.1	12	2	PN0581	tyrosine 3-monoxy	347	13	18.1	15	2	F28587	T-cell receptor be
275	13	18.1	12	2	PN0580	tyrosine 3-monoxy	348	13	18.1	15	2	PN0562	dystrrophin-associ
276	13	18.1	12	2	PN0579	tyrosine 3-monoxy	349	13	18.1	15	2	I53284	T-cell receptor be
277	13	18.1	12	2	PN0577	tyrosine 3-monoxy	350	13	18.1	15	2	PD0444	coupling factor 6
278	13	18.1	12	2	PN0576	tyrosine 3-monoxy	351	13	18.1	15	2	I78833	flit3 ligand isofor
279	13	18.1	12	2	PN0578	tyrosine 3-monoxy	352	13	18.1	15	2	PT0097	glutathione peroxi
280	13	18.1	12	2	S26557	T-cell receptor be	353	13	18.1	15	2	PH0789	T-cell receptor al
281	13	18.1	12	2	S26556	T-cell receptor be	354	13	18.1	15	2	PH0770	T-cell receptor be
282	13	18.1	12	2	S26558	T-cell receptor be	355	13	18.1	15	2	PH0764	T-cell receptor be
283	13	18.1	12	2	S26554	T-cell receptor be	356	13	18.1	15	2	PH1436	capaid protein Vp1
284	13	18.1	12	2	S26555	T-cell receptor be	357	13	18.1	15	2	PO0545	carbon-monoxide de
285	13	18.1	12	2	S36899	ribosomal protein	358	13	18.1	15	2	PL0143	GMP-binding protei
286	13	18.1	12	2	PA0019	acidic ribosomal p	359	13	18.1	15	2	T03000	ribonucleoside-dip
287	13	18.1	12	2	S67528	napin - rape (frag	360	13	18.1	15	2	A17340	ribosomal protein
288	13	18.1	12	2	S18722	matk protein -- bee	361	13	18.1	15	2	S36889	GLYMI - soybean
289	13	18.1	12	2	PH0746	T-cell receptor be	362	13	18.1	15	2	A56970	casein kinase II
290	13	18.1	12	2	PH0771	T-cell receptor be	363	13	18.1	15	2	B45133	transferrin prote
291	13	18.1	12	2	A49261	coagulation factor	364	13	18.1	15	2	C34874	acid phosphatase
292	13	18.1	12	2	S65409	histone H2B - huma	365	13	18.1	15	2	A56963	pyrogallol hydroxy
293	13	18.1	13	2	PO0491	self-incompatibili	366	13	18.1	15	2	S65429	avenin gamma-4 - c
294	13	18.1	13	2	E39778	lactose phosphotra	367	13	18.1	15	2	S29207	neuropeptide Led-c
295	13	18.1	13	2	B44957	protein L7 - commo	368	13	18.1	8	2	A44960	hypertrehalosemic
296	13	18.1	13	2	S09395	hypothetical prote	369	13	18.1	8	2	S08995	adipokinetic hormo
297	13	18.1	13	2	PT0331	Ig heavy chain CRD	370	13	18.1	8	2	A49823	adipokinetic hormo
298	13	18.1	13	2	D61458	Ig kappa chain V-I	371	13	18.1	8	2	A28804	nitrate reductase
299	13	18.1	13	2	B61458	Ig lambda chain V-	372	13	18.1	8	2	S68802	205K exantigen -
300	13	18.1	13	2	G61458	T-cell antigen rec	373	13	18.1	8	2	G33098	hypertrehalosemic
301	13	18.1	13	2	S47357	mannose-1-phosphat	374	13	18.1	8	2	A39892	hypertrehalosemic
302	13	18.1	13	2	B47415	Ig H chain V-D-J r	375	13	18.1	8	2	S45651	R-phycocerythrin ga
303	13	18.1	13	2	PH1593	T-cell receptor be	376	13	18.1	8	2	A37521	neuropeptide M-I -
304	13	18.1	13	2	PH1479	S-lucos specific g	377	13	18.1	8	2	A05169	apolipoprotein A-I
305	13	18.1	13	2	D56661	early nodulin 40 -	378	13	18.1	8	2	I48935	phyllinocerulein -
306	13	18.1	13	2	S60046	lymadFamide 4 - g	379	13	18.1	9	2	A61357	fibriнопептиде B -
307	13	18.1	13	2	S32474	lymadFamide 5 - g	380	13	18.1	9	2	D28854	macrophage chemota
308	13	18.1	13	2	S32475	probable sex-speci	381	13	18.1	10	2	A37027	6-phosphofructo-2-
309	13	18.1	13	2	B19434	cysteine proteinas	382	13	18.1	10	2	A43405	hypertrehalosemic
310	13	18.1	13	2	PC4391	hypothetical prote	383	13	18.1	10	2	S08997	hypertrehalosemic
311	13	18.1	13	2	G83988	serine proteinase	384	13	18.1	10	2	A60421	hypertrehalosemic
312	13	18.1	13	2	S66558	tryptophyllin-rela	385	13	18.1	10	2	S08998	hypertrehalosemic
313	13	18.1	13	2	S21152	bradykinin-like pe	386	13	18.1	10	2	A26381	hypertrehalosemic
314	13	18.1	13	2	A61361	tryp operon leader	387	13	18.1	10	2	A61337	caerulein - frog
315	13	18.1	14	1	LFECM	tryp operon leader	388	13	18.1	10	2	PT0322	Ig heavy chain CRD
316	13	18.1	14	1	PC2373	probable IMP dehyd	389	13	18.1	10	2	E41946	T-cell receptor ga
317	13	18.1	14	2	S21247	H+-transporting tw	390	13	18.1	10	2	D28027	protein P7 - curle
318	13	18.1	14	2	A01250	angiotensin precu	391	13	18.1	10	2	S62880	polygalacturonase
319	13	18.1	14	2	A49018	myosin heavy chain	392	13	18.1	10	2	PN0165	triose-phosphate i
320	13	18.1	14	2	E90858	trp operon leader	393	13	18.1	10	2	S53789	neuropeptide Pec-H
321	13	18.1	14	2	B85761	trp operon leader	394	13	18.1	10	2	D60787	sperm-activating p

395	12	16.7	10	2	E39572	sperm-activating p	468	12	16.7	15	2	PL0109	complement factor
396	12	16.7	10	2	D60589	sperm-activating p	469	12	16.7	15	2	A56049	urinary tract ston
397	12	16.7	10	2	A60588	sperm-activating p	470	12	16.7	15	2	PH1455	T-cell receptor al
398	12	16.7	11	2	A29806	acidic proline-rich	471	12	16.7	15	2	PC2374	unidentified 22k p
399	12	16.7	11	2	PT0218	T-cell receptor be	472	12	16.7	15	2	PA0093	emulatin synthetas
400	12	16.7	11	2	C49037	Tcr gamma V-J reql	473	12	16.7	15	2	PA0059	protein QF200021 -
401	12	16.7	11	2	S78422	ribosomal protein	474	12	16.7	15	2	PA0106	protein QF200076 -
402	12	16.7	11	2	I52304	gene rSSTR4 protei	475	12	16.7	15	2	A30330	neuropeptide pep -
403	12	16.7	11	2	I41138	acetyl ornithine d	476	12	16.7	15	2	I56046	urinary tract ston
404	12	16.7	11	2	I77447	urinary protein -	477	12	16.7	15	2	G24417	interphotoreceptor
405	12	16.7	11	4	PC2124	aminotransferase c	478	12	16.7	15	2	PT0096	pyruvate dehydroge
406	12	16.7	11	4	I52708	ELAV-like neuronal	479	12	16.7	15	2	PQ0780	NADH2 dehydrogena
407	12	16.7	12	2	C36201	1-aminocyclopropan	480	12	16.7	11	15.3	I54357	schwannomin - mous
408	12	16.7	12	2	PH1675	Ig heavy chain V r	481	12	16.7	11	15.3	PL0146	carbon-monoxide de
409	12	16.7	12	2	S25056	Ig heavy chain - m	482	11	15.3	4	2	PT0551	T-cell receptor be
410	12	16.7	12	2	S11298	hemagglutinin prec	483	11	15.3	5	1	HOB0HA	protoclin - Americ
411	12	16.7	12	2	A26093	microbial collagen	484	11	15.3	5	2	A44955	alkenal monooxygen
412	12	16.7	12	2	S74196	3-hydroxy-3-methyl	485	11	15.3	5	2	B22565	R-phycoerythrin al
413	12	16.7	12	2	S68402	NAD(+)-glycohydrol	486	11	15.3	5	2	PQ0009	angiotensin-conver
414	12	16.7	12	2	PH1581	Ig H chain V-D-J r	487	11	15.3	5	2	A60521	glycogen phosphory
415	12	16.7	12	2	H41946	T-cell receptor ga	488	11	15.3	5	2	A60411	proctolin - Atlant
416	12	16.7	12	2	PH1457	T-cell receptor be	489	11	15.3	6	2	S02617	alcohol dehydrogen
417	12	16.7	12	2	PH1459	T-cell receptor be	490	11	15.3	6	2	B44510	hypothetical prote
418	12	16.7	12	2	S07206	kassinin - Senegal	491	11	15.3	6	2	I37263	hypothetical prote
419	12	16.7	13	2	A60856	limbin alpha chai	492	11	15.3	6	2	I65546	Y protein - human
420	12	16.7	13	2	PH1676	Ig heavy chain V r	493	11	15.3	6	2	I59142	MHC H2-L antigen -
421	12	16.7	13	2	S15755	actin 7 - soybean	494	11	15.3	6	2	A41946	platelet-derived g
422	12	16.7	13	2	S38736	lipid transfer pro	495	11	15.3	6	2	I49424	T-cell receptor ga
423	12	16.7	13	2	S28425	20K protein - rape	496	11	15.3	7	2	E61491	cytotoxic T-Lympo
424	12	16.7	13	2	E60396	antigen 7H8/2 - ma	497	11	15.3	7	2	S70335	seed protein ws-5
425	12	16.7	13	2	A33660	osteoclast functio	498	11	15.3	7	2	S78024	endosperm protein,
426	12	16.7	13	2	PT0256	Ig heavy chain CRD	499	11	15.3	7	2	A11483	ribosomal protein,
427	12	16.7	13	2	S47376	T-cell antigen rec	500	11	15.3	7	2	B33541	aspartate transam
428	12	16.7	13	2	S47383	T-cell antigen rec	501	11	15.3	7	2	PT0520	hypothetical prote
429	12	16.7	13	2	B56864	dipeptidyl-peptida	502	11	15.3	7	2	PT0586	T-cell receptor be
430	12	16.7	13	2	A40207	cell surface glyco	503	11	15.3	7	2	PT0581	T-cell receptor be
431	12	16.7	13	2	A61514	glutathione transf	504	11	15.3	8	2	S63493	disulfamatory sulf
432	12	16.7	13	2	S09018	hemolytic protein	505	11	15.3	8	2	PT0311	Ig heavy chain CRD
433	12	16.7	13	2	H85575	hypothetical prote	506	11	15.3	8	2	PN0043	phosphatidylethano
434	12	16.7	14	2	C40944	hypothetical prote	507	11	15.3	8	2	PL0162	paramyosin - north
435	12	16.7	14	2	A60622	somostatin - spo	508	11	15.3	8	2	S66646	cardioacceleratory
436	12	16.7	14	2	PH1677	Ig heavy chain V r	509	11	15.3	8	2	A42689	major postsynaptic
437	12	16.7	14	2	S60353	amylopullulanase -	510	11	15.3	8	2	A35180	neutral proteinase
438	12	16.7	14	2	S35267	acetyl-CoA carboxy	511	11	15.3	9	2	A93408	oxytocin - Austral
439	12	16.7	14	2	PH1769	T cell receptor al	512	11	15.3	9	2	A92774	oxytocin - spotted
440	12	16.7	14	2	PH1626	Ig H chain V-D-J r	513	11	15.3	9	2	A93147	oxytocin - finback
441	12	16.7	14	2	PH0800	T-cell receptor al	514	11	15.3	9	2	A91466	oxytocin - hippo
442	12	16.7	14	2	C48394	major fat-globule	515	11	15.3	9	2	B90667	oxytocin - rabbit
443	12	16.7	14	2	B56819	PS I complex subun	516	11	15.3	9	2	E28854	fibriopeptide B -
444	12	16.7	14	2	S33801	chaperone, TCP1-re	517	11	15.3	9	2	PT0268	Ig heavy chain CRD
445	12	16.7	14	2	PS0249	porin - rice (stra	518	11	15.3	9	2	PT0324	Ig heavy chain CRD
446	12	16.7	14	2	B60683	malate dehydrogena	519	11	15.3	9	2	B46250	alpha-adaptin - bo
447	12	16.7	14	2	PC4376	telomeric and tetr	520	11	15.3	9	2	PH1591	Ig H chain V-D-J r
448	12	16.7	14	2	S29878	Na+/K+-exchanging	521	11	15.3	9	2	J01202	leader peptide - p
449	12	16.7	14	4	I52618	hemoglobin beta ch	522	11	15.3	10	1	XASNPC	angiotensin-conver
450	12	16.7	15	2	A47146	topoisomerase I -	523	11	15.3	10	2	S71868	glutathione transf
451	12	16.7	15	2	C37765	hypothetical prote	524	11	15.3	10	2	S66458	ferridoxin - Rhizo
452	12	16.7	15	2	PA0016	glycine cleavage T	525	11	15.3	10	2	S48182	bacterioferritin -
453	12	16.7	15	2	PA0046	protein QAI00044 -	526	11	15.3	10	2	JP0072	ribosomal protein
454	12	16.7	15	2	PA0009	seed storage prote	527	11	15.3	10	2	PT0038	glutathione transf
455	12	16.7	15	2	PS0208	20K protein 5403 -	528	11	15.3	10	2	C61440	polygalacturonase
456	12	16.7	15	2	PA0052	protein QF200015 -	529	11	15.3	10	2	C39111	Ig heavy chain C r
457	12	16.7	15	2	PA0051	protein QF200016 -	530	11	15.3	10	2	PT0243	Ig heavy chain CRD
458	12	16.7	15	2	PT0222	Ig heavy chain CDR	531	11	15.3	10	2	S23371	T-cell receptor al
459	12	16.7	15	2	PH1366	Ig heavy chain DY	532	11	15.3	10	2	I48778	small nuclear ribo
460	12	16.7	15	2	PH1318	Ig heavy chain DY	533	11	15.3	10	2	PH0807	T-cell receptor al
461	12	16.7	15	2	S55312	TSH protein beta c	534	11	15.3	10	2	D54823	olfactory receptor
462	12	16.7	15	2	A27504	histone H2A - mous	535	11	15.3	10	2	S65715	aryl hydrocarbon (
463	12	16.7	15	2	PH1616	Ig H chain V-D-J r	536	11	15.3	10	2	S65385	cytochrome-c oxida
464	12	16.7	15	2	PH1619	Ig H chain V-D-J r	537	11	15.3	10	2	C35389	urase (EC 3.5.1.5
465	12	16.7	15	2	PH0775	T-cell receptor al	538	11	15.3	10	2	A44646	neurotoxin-associa
466	12	16.7	15	2	PH0779	T-cell receptor al	539	11	15.3	10	2	I44644	neurotoxin-associa
467	12	16.7	15	2	A49887	transcription fact	540	11	15.3	10	2		

541	11	15.3	10	2	S38305	614	11	15.3	13	2	PT0305	Ig heavy chain CRD
542	11	15.3	10	2	PX0030	615	11	15.3	13	2	S70441	pancreatic elastase
543	11	15.3	10	2	B61440	616	11	15.3	13	2	S47378	T-cell antigen rec
544	11	15.3	10	2	S43630	617	11	15.3	13	2	S23372	T-cell receptor al
545	11	15.3	10	2	S43631	618	11	15.3	13	2	S10562	zona pellucida-bin
546	11	15.3	10	2	A30823	619	11	15.3	13	2	B25448	Ig kappa-1 chain,
547	11	15.3	10	2	F33932	620	11	15.3	13	2	A32486	beta protein - rat
548	11	15.3	10	2	C54823	621	11	15.3	13	2	D47630	Ig kappa chain J r
549	11	15.3	10	2	A61318	622	11	15.3	13	2	S03063	Ig lambda chain J
550	11	15.3	10	2	B61318	623	11	15.3	13	2	A59387	VCAM-1 5'UTR bindi
551	11	15.3	10	2	T13838	624	11	15.3	13	2	A32453	phloroglucinol red
552	11	15.3	10	2	T12312	625	11	15.3	13	2	G22565	R-phycocerythrin ga
553	11	15.3	10	2	PQ0785	626	11	15.3	13	2	S14316	photosystem I 9K c
554	11	15.3	10	2	PQ0783	627	11	15.3	13	2	S09733	photosystem I prot
555	11	15.3	10	2	C60787	628	11	15.3	13	2	D61491	seed protein I prot
556	11	15.3	10	2	C60588	629	11	15.3	13	2	PQ0700	unidentified 6.3/4
557	11	15.3	10	2	E60527	630	11	15.3	13	2	G56046	urinary tract ston
558	11	15.3	10	2	S07202	631	11	15.3	13	2	S32551	glutathione transf
559	11	15.3	10	2	C61033	632	11	15.3	14	2	S22236	lipoxygenase (EC 1
560	11	15.3	10	2	B61033	633	11	15.3	14	2	S62374	alpha-1-antichymot
561	11	15.3	10	2	S27178	634	11	15.3	14	2	PA0109	porin por 1B - Ara
562	11	15.3	10	2	C45474	635	11	15.3	14	2	B56863	photosystem I reac
563	11	15.3	11	1	EC042M	636	11	15.3	14	2	A61002	photosystem II oxy
564	11	15.3	11	1	PN0042	637	11	15.3	14	2	E33098	214K exoantigen (v
565	11	15.3	11	2	A40693	638	11	15.3	14	2	PL0152	metal-binding prot
566	11	15.3	11	2	E60691	639	11	15.3	14	2	S38307	DEB-A protein - fr
567	11	15.3	11	2	A34135	640	11	15.3	14	2	A60770	cell surface alloca
568	11	15.3	11	2	PT0301	641	11	15.3	14	2	PH1348	Ig heavy chain DJ
569	11	15.3	11	2	S68649	642	11	15.3	14	2	PH1322	Ig heavy chain DJ
570	11	15.3	11	2	S45386	643	11	15.3	14	2	PH1311	Ig heavy chain DJ
571	11	15.3	11	2	S35490	644	11	15.3	14	2	S47366	T-cell antigen rec
572	11	15.3	11	2	B39853	645	11	15.3	14	2	S23369	T-cell receptor al
573	11	15.3	11	2	A55149	646	11	15.3	14	2	PH0135	T-cell receptor be
574	11	15.3	11	2	S33519	647	11	15.3	14	2	B28018	very late antigen-
575	11	15.3	11	2	C61497	648	11	15.3	14	2	A43847	Ig mu chain V regl
576	11	15.3	11	2	S19775	649	11	15.3	14	2	JS0272	hypothetical 1.5K
577	11	15.3	11	2	PC4267	650	11	15.3	14	2	PH1614	Ig H chain V-D-J r
578	11	15.3	11	2	A26120	651	11	15.3	14	2	PH1617	Ig H chain V-D-J r
579	11	15.3	11	2	S21727	652	11	15.3	14	2	PH1623	Ig H chain V-D-J r
580	11	15.3	11	2	A14454	653	11	15.3	14	2	PH1608	Ig H chain V-D-J r
581	11	15.3	11	2	A34243	654	11	15.3	14	2	PH0792	T-cell receptor al
582	11	15.3	11	2	S23306	655	11	15.3	14	2	S29632	xylin 1,4-Beta-xy1
583	11	15.3	12	1	A43975	656	11	15.3	14	2	PA0045	porin por1 - Arabi
584	11	15.3	12	1	S11286	657	11	15.3	14	2	PN0147	omega-gliadin 1 a
585	11	15.3	12	2	I64829	658	11	15.3	14	2	PT0029	karatsasin - karata
586	11	15.3	12	2	S26559	659	11	15.3	14	2	S45655	cathepsin L (EC 3,
587	11	15.3	12	2	C39109	660	11	15.3	14	2	S00150	ovostatin - duck (
588	11	15.3	12	2	C64030	661	11	15.3	15	1	B36079	hypothetical prote
589	11	15.3	12	2	S49547	662	11	15.3	15	1	SFRF	scotophobin - rat
590	11	15.3	12	2	PH1324	663	11	15.3	15	1	NTKNAG	alpha-conotoxin GI
591	11	15.3	12	2	PH1308	664	11	15.3	15	2	PA0041	plastoquinol-plast
592	11	15.3	12	2	S47393	665	11	15.3	15	2	B61243	dimethylamline mo
593	11	15.3	12	2	S47394	666	11	15.3	15	2	S14749	3-dehydroquinase -
594	11	15.3	12	2	PH1183	667	11	15.3	15	2	PQ0195	Sfl1-glycoprotein
595	11	15.3	12	2	S74144	668	11	15.3	15	2	S21240	alpha-glucosidase
596	11	15.3	12	2	PH1587	669	11	15.3	15	2	S21241	oligo-1,6-glucosid
597	11	15.3	12	2	S39762	670	11	15.3	15	2	PC2215	fibrogenolytic p
598	11	15.3	12	2	PH0920	671	11	15.3	15	2	A22789	platelet-derived g
599	11	15.3	12	2	PH1467	672	11	15.3	15	2	A49155	vasotocin-associat
600	11	15.3	12	2	PH1458	673	11	15.3	15	2	PH1319	Ig heavy chain DJ
601	11	15.3	12	2	PH1466	674	11	15.3	15	2	S26527	T-cell receptor al
602	11	15.3	12	2	S71034	675	11	15.3	15	2	PS0382	Ig heavy chain J r
603	11	15.3	12	2	PA0047	676	11	15.3	15	2	B56661	S-locus specific g
604	11	15.3	12	2	PN0162	677	11	15.3	15	2	PA0034	protein QA300024 -
605	11	15.3	12	2	PA0098	678	11	15.3	15	2	S29386	nigericin - Desu
606	11	15.3	12	2	A61503	679	11	15.3	15	2	A56863	phycocerythrin I
607	11	15.3	12	2	B32521	680	11	15.3	15	2	T46625	hypothetical prote
608	11	15.3	12	2	F84132	681	11	15.3	15	2	PA0014	seed storage prote
609	11	15.3	13	1	UNBO	682	11	15.3	15	2	PN0173	seed storage prote
610	11	15.3	13	1	UNOBT	683	11	15.3	15	2	S13973	chlorophyll a/b-bi
611	11	15.3	13	2	A53608	684	11	15.3	15	2	S08209	hypothetical prote
612	11	15.3	13	2	H44957	685	11	15.3	15	2	S62620	protein disulfide-
613	11	15.3	13	2	A23694	686	11	15.3	15	2	PQ0192	stylar glycoprotei

687	11	15.3	15	2	PQ0193	stylar glycoprotei
688	11	15.3	15	2	PA0095	protein QF200056 -
689	11	15.3	15	2	PN0144	serine proteinase
690	11	15.3	15	2	S10388	Ig heavy chain J r
691	11	15.3	15	2	S10386	Ig heavy chain J r
692	11	15.3	15	2	B41436	ovostatin - green
693	11	15.3	15	2	S60007	glial hyaluronate-
694	11	15.3	15	2	PH1314	Ig heavy chain DJ
695	11	15.3	15	2	PH1320	Ig heavy chain DJ
696	11	15.3	15	2	PH1762	T cell receptor al
697	11	15.3	15	2	PH1788	T cell receptor al
698	11	15.3	15	2	S47367	T-cell antigen rec
699	11	15.3	15	2	A49252	T-cell receptor be
700	11	15.3	15	2	PH0136	T-cell receptor be
701	11	15.3	15	2	B56046	urinary tract ston
702	11	15.3	15	2	F44823	synaptosomal-assoc
703	11	15.3	15	2	PH1610	Ig H chain V-D-J r
704	11	15.3	15	2	PH1378	T antigen variant
705	11	15.3	15	2	PH1377	T antigen variant
706	11	15.3	15	2	PH0808	T-cell receptor al
707	11	15.3	15	2	B26501	lipoprotein lipase
708	11	15.3	15	2	S72431	epoxypropan isomer
709	11	15.3	15	2	PT0091	H+-transporting tw
710	11	15.3	15	2	PQ0778	NADH2 dehydrogenas
711	11	15.3	15	2	S61438	hypothetical prote
712	11	15.3	15	2	PH0216	asparase (EC 3.2.1.
713	11	15.3	15	2	A41338	isocitrate lyase (
714	11	15.3	15	2	A26228	spot 42 protein -
715	11	15.3	15	2	C43334	orf3 3' to aadr -
716	11	15.3	15	2	S03353	plastocyanin - Mic
717	11	15.3	15	2	S36890	ribosomal protein
718	11	15.3	15	2	A40634	orf19 3' of eryK -
719	11	15.3	15	2	A48372	benzoyl-CoA ligase
720	11	15.3	15	2	PA0036	glycine cleavage s
721	11	15.3	15	2	PA0005	lectin A1 - psopio
722	11	15.3	15	2	PA0006	lectin A3 - psopio
723	11	15.3	15	2	PS0450	23k protein 4307 -
724	11	15.3	15	2	PS0455	superoxide dismuta
725	11	15.3	15	2	PA0105	heat shock protein
726	11	15.3	15	2	PA0071	superoxide dismuta
727	11	15.3	15	2	B49177	21k protein p2, mi
728	11	15.3	15	2	A49177	22k protein p1, mi
729	11	15.3	15	2	A36279	chemoattractant pr
730	11	15.3	15	2	PC1313	small granule S6 c
731	11	15.3	15	2	A61612	allatostatin - cob
732	11	15.3	15	2	PT0090	alpha-glucosidase
733	11	15.3	15	2	S77988	cytochrome-c oxida
734	11	15.3	15	2	B45115	peptidylprolyl iso
735	11	15.3	15	2	A35417	28k serine protein
736	11	15.3	15	2	I46909	voltage-dependent
737	11	15.3	15	2	PT0094	succinate dehydrog
738	11	15.3	15	2	S04586	NADH2 dehydrogenas
739	11	15.3	15	4	I38032	hypothetical MN1/T
740	11	15.3	15	4	I38031	hypothetical MN1/T
741	11	15.3	15	4	I38888	COI intron 16 prot
742	10	13.9	4	2	PT0240	Ig heavy chain CRD
743	10	13.9	4	2	A53284	T-cell receptor be
744	10	13.9	4	2	PT0721	T-cell receptor be
745	10	13.9	4	2	A32039	tyrosine-melanocyt
746	10	13.9	5	2	B37325	pap fibribrial regul
747	10	13.9	5	2	S11127	phosphoprotein, bo
748	10	13.9	5	2	D44823	synaptosomal-assoc
749	10	13.9	5	2	PT0625	T-cell receptor be
750	10	13.9	5	2	PT0660	T-cell receptor be
751	10	13.9	6	2	PT0713	T-cell receptor be
752	10	13.9	6	2	A60494	antineoplastic gly
753	10	13.9	6	2	H48394	glycoprotein compo
754	10	13.9	6	2	B26206	alpha-1,4-glucan-p
755	10	13.9	6	2	A20186	fatty-acid synthas
756	10	13.9	6	2	PT0519	T-cell receptor be
757	10	13.9	6	2	PT0643	T-cell receptor be
758	10	13.9	6	2	PT0621	T-cell receptor be
759	10	13.9	6	2	PT0560	T-cell receptor be

760	10	13.9	6	2	PT0718	T-cell receptor be
761	10	13.9	6	2	PT0727	T-cell receptor be
762	10	13.9	6	2	PT0730	T-cell receptor be
763	10	13.9	6	2	PD0028	pev-kinin 2 - pena
764	10	13.9	6	2	A61068	locustactinin - mig
765	10	13.9	6	2	S55548	mech protein - Esc
766	10	13.9	7	2	S42407	gramicidin S synth
767	10	13.9	7	2	A33098	244k exoantigen -
768	10	13.9	7	2	PT0246	Ig heavy chain CRD
769	10	13.9	7	2	PH1602	Ig H chain V-D-J r
770	10	13.9	7	2	PT0521	T-cell receptor be
771	10	13.9	7	2	PT0663	T-cell receptor be
772	10	13.9	7	2	PT0579	T-cell receptor be
773	10	13.9	7	2	PD0029	pev-kinin 1 - pena
774	10	13.9	7	2	S29735	polyphosphate-gluc
775	10	13.9	7	2	T09512	NADH2 dehydrogenas
776	10	13.9	7	2	PT0529	T-cell receptor be
777	10	13.9	7	2	A61081	cryptophyllin, bas
778	10	13.9	8	2	S11545	adipokinetic hormo
779	10	13.9	8	2	A61348	red pigment-concen
780	10	13.9	8	2	A43976	hypertrethaloemic
781	10	13.9	8	2	B43975	hypertrethaloemic
782	10	13.9	8	2	T10952	hypothetical prote
783	10	13.9	8	2	S13661	polygalacturonase
784	10	13.9	8	2	PT0368	Ig gamma chain C r
785	10	13.9	8	2	PT0323	Ig heavy chain CRD
786	10	13.9	8	2	B45800	serum albumin - do
787	10	13.9	8	2	PT0627	T-cell receptor be
788	10	13.9	8	2	PT0559	T-cell receptor be
789	10	13.9	8	2	PT0554	T-cell receptor be
790	10	13.9	8	2	PT0716	T-cell receptor be
791	10	13.9	8	2	PT0725	T-cell receptor be
792	10	13.9	8	2	PC4372	telomerase and tetr
793	10	13.9	8	2	S65647	2-hydroxyglutaryl-
794	10	13.9	8	2	PT0030	inlinase (EC 3.2.
795	10	13.9	8	2	US0315	leucokinin V - Mad
796	10	13.9	8	2	US0317	leucokinin VII - M
797	10	13.9	8	2	E47393	neuropeptide calla
798	10	13.9	8	2	A59028	MHC class I histoc
799	10	13.9	8	4	I54017	granulocyte-colony
800	10	13.9	9	2	A44873	caldesmon - rabbit

ALIGNMENTS

RESULT 1

PH0774 T-cell receptor beta chain (RF3.10.3) - mouse (fragment)

C,Species: Mus musculus (house mouse)

C,Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C,Accession: PH0774

R,Cananova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J,Exp. Med. 174, 1371-1383, 1991

A,Title: T cell receptor genes in a series of class I major histocompatibility complex-r alleles exclusion and antigen-specific repertoire.

A,Reference number: PH0746; MUID:92078846; PMID:1836010

A,Accession: PH0774

A,Molecule type: mRNA

A,Residues: 1-14 <CAS>

A,Cross-references: UNIPARC:UP10000115FC1; EMBL:X60870; NID:G53975; PIDN:CAA43258.1; PID

A,Experimental source: T lymphocyte

C,Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 3.2e+02;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 SVAKSVSLVNG 15

Db 3 SSSASAEVLVNG 14

RESULT 2

C59137

protein pf3 - golden needle mushroom (fragment)

C/Species: Flammulina velutipes (golden needle mushroom)

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: C59137

R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.

submitted to the Protein Sequence Database, November 1999

A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr

A/Reference number: A59137

A/Accession: C59137

A/Molecule type: protein

A/Residues: 1-14 <SAKS>

A/Cross-references: UNIPROT:Q7M4W9; UNIPARC:UPI000017CB24

Query Match

Best Local Similarity 34.7%; Score 25; DB 2; Length 14;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSVA 6

DB 9 VPSIS 14

RESULT 3

S49409

H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Streptococcus oralis (fragment

C/Species: Streptococcus oralis

C/Date: 29-Nov-1995 #sequence_revision 01-Aug-1997 #text_change 31-Dec-2004

C/Accession: S49409; S38211

R/Fenoll, A.; Munoz, R.; Garcia, E.; de la Campa, A.G.

Mol. Microbiol. 12, 587-598, 1994

A/Title: Molecular basis of the optochin-sensitive phenotype of pneumococcus: characteri

ases.

A/Reference number: S49398; MID:95020593; PMID:7934862

A/Accession: S49409

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-15 <FEN>

A/Cross-references: UNIPROT:Q60249; UNIPARC:UPI0000170206; EMBL:Z26853; NID:9407180; PID

C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match

Best Local Similarity 33.3%; Score 24; DB 2; Length 15;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VMSLYIG 15

DB 1 LSSMYIG 7

RESULT 4

A44871

monodehydroascorbate reductase (NADH2) (EC 1.6.5.4) - soybean (fragment)

C/Species: Glycine max (soybean)

C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A44871

R/Dalton, D.A.; Langeberg, L.; Robbins, M.

Arch. Biochem. Biophys. 292, 281-286, 1992

A/Title: Purification and characterization of monodehydroascorbate reductase from soybea

A/Reference number: A44871; MID:92088257; PMID:1727643

A/Accession: A44871

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <DAL>

A/Cross-references: UNIPROT:Q9S926; UNIPARC:UPI000009DB60

A/Experimental source: root nodules, cv. Williams

A/Note: sequence extracted from NCBI backbone (NCBIP:71052)

C/Keywords: oxidoreductase

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLYIG 15

DB 1 AKTFKXIIIG 10

RESULT 5

S47372

T-cell antigen receptor V β junction beta chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C/Accession: S47372

R/Lehner, P.U.

submitted to the EMBL Data Library, August 1994

A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T

A/Reference number: S47355

A/Accession: S47372

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-13 <LEH>

A/Cross-references: UNIPARC:UPI0000116684; EMBL:Z35697; NID:9527485; PID:CAA84766.1; P

Query Match

Best Local Similarity 31.9%; Score 23; DB 2; Length 13;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13

DB 2 ASSIRSAV 9

RESULT 6

JN0390

histamine-releasing peptide II - oriental hornet

N/Alternate names: venom protein HR-2

C/Species: Vespa orientalis (oriental hornet)

C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004

C/Accession: JN0390; S10919

R/Miroshnikov, A.I.; Shezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gu

Bioorg. Khim. 7, 1467-1477, 1981

A/Title: Structure and properties of histamine releasing peptides from the venom of Vespa

A/Reference number: JN0389

A/Accession: JN0390

A/Molecule type: protein

A/Residues: 1-14 <MIR>

A/Cross-references: UNIPROT:P17236; UNIPARC:UPI0000035436

R/Tuchibaev, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1988

A/Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S

A/Reference number: S06445

A/Accession: S10919

A/Molecule type: protein

A/Residues: 1-14 <TUI>

A/Cross-references: UNIPARC:UPI0000035436

C/Superfamily: crabrolin

C/Keywords: amidated carboxyl end; venom

F/14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match

Best Local Similarity 31.9%; Score 23; DB 2; Length 14;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPSVAKSVKSL 12

DB 2 LPLILGKLVKGL 13

RESULT 7

G61308

hemocyanin chain 3C - Sahara scorpion (fragment)

C/Species: Androctonus australis (Sahara scorpion)

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C/Accession: G61308
C/Species: J.; Jolles, P.; Lamy, J.; Lamy, J.
C/Date: 106, 289-291, 1979
C/Title: Structural characterization of seven different subunits in Androctonus australis
C/Accession: A61308; MUID:80047238; PMID:499512
A/Reference number: G61308
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <JOL>
A/Cross-references: UNIPROT:Q7M487; UNIPARC:UPI000017BE01

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 25.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSLY 13
|:|:|:
Db 2 PINIQRIITSLF 13

RESULT 8

S47365
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47365
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35690; NID:G527471; PIDN:CAA84759.1; PI
A/Accession: S47375
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE2>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35700; NID:G527493; PIDN:CAA84769.1; PI
A/Accession: S47379
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE3>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35708; NID:G527509; PIDN:CAA84777.1; PI
A/Accession: S47396
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE4>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35674; NID:G527527; PIDN:CAA84743.1; PI
A/Accession: S47397
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE5>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35675; NID:G527529; PIDN:CAA84744.1; PI
A/Accession: S47398
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE6>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
C/Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AKSVKSLY 13
|:|:|:
Db 2 ASSIRSSY 9

RESULT 9

S43634
Cytochrome-c oxidase (EC 1.9.3.1) chain VIIC, cardiac - rainbow trout (fragment)
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C/Accession: S43634
C/Reference number: S43634
A/Status: preliminary
A/Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome
A/Reference number: S43624; MUID:94237150; PMID:8181469
A/Accession: S43634
A/Molecule type: protein
A/Residues: 1-15 <PRE>
A/Cross-references: UNIPARC:UPI000017BF5A
A/Note: the source is designated as Salmo gairdneri
C/Genetics:
A/Genome: nuclear
C/Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoredu

Query Match 30.6%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|:|:|:
Db 11 LPFSV 15

RESULT 10

E45691
Probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lact
C/Species: Lactobacillus delbrueckii subsp. lactis phase LU-H
C/Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
C/Accession: E45691
R/Vasala, A.; Dupont, L.; Baumann, M.; Ritzenhaller, P.; Alcossega, T.
J. Virol. 67, 3061-3068, 1993
A/Title: Molecular comparison of the structural proteins encoding gene clusters of two r
A/Reference number: A45691; MUID:93267750; PMID:8497043
A/Accession: E45691
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-12 <VAS>
A/Cross-references: UNIPROT:O04769; UNIPARC:UPI000017986E
A/Note: sequence extracted from NCBI Backbone (NCBIN:132363, NCBI:132373)
C/Superfamily: uncharacterized conserved protein

Query Match 27.8%; Score 20; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 2.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFVS 8
|:|:|:
Db 5 IPYQWAVS 12

RESULT 11

S47360
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47360
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47360
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <LEH>
A/Cross-references: UNIPARC:UPI000011667A; EMBL:Z35684; NID:G527457; PIDN:CAA84753.1; PI
C/Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSL 12
| | | |
Db 6 AKSISL 12

RESULT 12

S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C:Accession: S47374; S47399; S47364
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116674; EMBL:Z35699; NID:9527491; PIDD:CAA84768.1; PI
A:Accession: S47399
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>
A:Cross-references: UNIPARC:UPI0000116674; EMBL:Z35677; NID:9527533; PIDD:CAA84746.1; PI
C:Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
| | | | |
Db 2 ASSMKRSSY 9

RESULT 13

I70075
glycophorin B (mistranslated) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 14-Aug-1997 #text_change 09-Jul-2004
C:Accession: I70075
R:Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.
J. Biol. Chem. 265, 9259-9263, 1990
A:Title: Identification of the crossing-over point of a hybrid gene encoding human glyco
A:Reference number: I55334; MUID:90264417; PMID:1971625
A:Accession: I70075
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-13 <REA>
A:Cross-references: UNIPROT:Q14461; UNIPARC:UPI00000730D2; GB:M3505; GB:005465; NID:g18
A:Note: this sequence was not determined in this report; the translation is from an inco
C:Genetics:
A:Gene: GDB:GYPB
A:Cross-references: GDB:118891
A:Map position: 4q28-4q31

Query Match 27.8%; Score 20; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVKSLY 13
| | | | |
Db 7 STVSLY 12

RESULT 14

A61362
bradykinin-like peptide III - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004

C:Accession: A61362

R:Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata
A:Reference number: A61362; MUID:69117202; PMID:5751736
A:Accession: A61362
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <NKA>
A:Cross-references: UNIPROT:Q7LZ53; UNIPARC:UPI000017A4F1
C:Keywords: skin

Query Match 27.8%; Score 20; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVA 6
| | | |
Db 7 PFRVA 11

RESULT 15

S68033
cytochrome P450 1A1 - tilapia (fragment)
C:Species: Oreochromis niloticus x Oreochromis aureus (tilapia)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S68033
R:Deng, Y.F.; Deng, T.H.
Arch. Biochem. Biophys. 322, 347-356, 1995
A:Title: Induction and purification of cytochrome P450 1A1 from 3-methylcholanthrene-tr
A:Reference number: S68033; MUID:96032654; PMID:7574707
A:Accession: S68033
A:Molecule type: protein
A:Residues: 1-10 <UEN>
A:Cross-references: UNIPARC:UPI000017CA77
A:Experimental source: liver and gill

Query Match 26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSV 9
| | | | |
Db 2 LPTIGALSV 10

RESULT 16

B43669
hypothetical protein (rhdA 5' region) - Synecchococcus sp. (fragment)
C:Species: Synecchococcus sp.
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C:Accession: B43669
R:Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.
J. Bacteriol. 173, 2751-2760, 1991
A:Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasm
A:Reference number: A43669; MUID:91210163; PMID:1708376
A:Accession: B43669
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <LAU>
A:Cross-references: UNIPARC:UPI000017ABB7; GB:M65244

Query Match 26.4%; Score 19; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKS 8
| | | | |
Db 2 PSSAAKN 8

RESULT 17

S26552

T-cell receptor beta chain (clone Cw3/701.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #ext_change 17-Mar-1999
C:Accession: S26552
R:Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26552
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI00001769C8; EMBL:X68002
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 18
S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #ext_change 17-Mar-1999
C:Accession: S26549; S26550
R:Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26549
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI00001769C9; EMBL:X67999
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A:Accession: S26550
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: UNIPARC:UPI00001769C9; EMBL:X68000
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 19
S26553
T-cell receptor beta chain (clone Cw3/56.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #ext_change 17-Mar-1999
C:Accession: S26553
R:Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26553
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI00001769C6; EMBL:X68003
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/56.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 20
PH1469
T-cell receptor beta chain (clone A3/H2R2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #ext_change 15-Mar-2004
C:Accession: PH1469; S26551
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Panmetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1469
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI000017C7A2
A:Experimental source: cytolytic T-lymphocyte, clone A3/H2R2
R:Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26551
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: UNIPARC:UPI000017C7A2; EMBL:X68001
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/1F11
C:Keywords: receptor; T-cell

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 21
S09721
2S albumin small chain nIII - rape (fragments)
C:Species: Brassica napus (rape)
C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #ext_change 13-Mar-1998
C:Accession: S09721
R:Monnaie, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09721
A:Molecule type: protein
A:Residues: 1-9;10-14 <MON>
A:Cross-references: UNIPARC:UPI000017B026; UNIPARC:UPI000017B027
A:Experimental source: seed

Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPSVAK 7
|||
Db 4 PPRIPK 9

RESULT 22

A44920
2-halobenzoate 1,2-dioxygenase component A beta chain - Pseudomonas cepacia (fragment)
C/Species: Pseudomonas cepacia
C/Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A44920
R/Refzner, S.; Muller, R.; Lingens, F.
J. Bacteriol. 174, 279-290, 1992
A/Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-comp
A/Reference number: A44920; MUID:92104974; PMID:1370284
A/Contents: 2CBS
A/Accession: A44920
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <P>
A/Cross-references: UNIPROT:Q9R506; UNIPARC:UPI000008BPBA
A/Note: sequence extracted from NCBI backbone (NCBIP:75379)

Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVKSLYL 14
Db 2 SLESSYL 8

RESULT 23
JN0859
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
C/Species: Sarda orientalis (striped bonito)
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C/Accession: JN0859
R/Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A/Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A/Reference number: JN0859; MUID:94080036; PMID:7764272
A/Accession: JN0859
A/Molecule type: protein
A/Residues: 1-7 <MAT>
A/Cross-references: UNIPARC:UPI00001566C2
A/Experimental source: intestine
C/Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin
C/Superfamily: bradykinin-potentiating peptide
C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.0%; Score 18; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 SVKSVK 10
Db 1 SVAKLEK 7

RESULT 24
A60624
angiotensin I - Japanese quail
C/Species: Coturnix coturnix japonica (Japanese quail)
C/Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 05-Oct-2004
C/Accession: A60624
R/Takel, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A/Title: Vasopressor and depressor effects of native angiotensins and inhibition of the
A/Reference number: A60624; MUID:90284684; PMID:2191893
A/Accession: A60624
A/Molecule type: protein
A/Residues: 1-10 <TKA>
A/Cross-references: UNIPROT:P01018; UNIPARC:UPI0000035278
C/Superfamily: serpin
C/Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 25.0%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 PFSV 5
Db 7 PFSL 10

RESULT 25
A90917
angiotensin precursor - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004
C/Accession: A90917; A01250
R/Nakayama, T.; Nakajima, T.; Sokane, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A/Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and it.
A/Reference number: A90917; MUID:74127845; PMID:4361802
A/Accession: A90917
A/Molecule type: protein
A/Residues: 1-10 <NAK>
A/Cross-references: UNIPROT:P01018; UNIPARC:UPI0000035278
C/Keywords: blood pressure control; hormone; vasoconstrictor
F/1-10/Product: angiotensin I #status experimental <ANI>
F/1-8/Product: angiotensin II #status experimental <AN2>

Query Match 25.0%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSV 5
Db 7 PFSL 10

RESULT 26
PH1375
T antigen variant K-2 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C/Accession: PH1375
R/Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for c
A/Reference number: PH1373; MUID:92364547; PMID:1380062
A/Accession: PH1375
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-11 <LIL>
A/Cross-references: UNIPARC:UPI000017C758

Query Match 25.0%; Score 18; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 KSVKSLYL 14
Db 2 KGVNMYL 9

RESULT 27
S21163
NAD ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
C/Accession: S21163
R/Potvin, F.; Thibodeau, J.; Kirkland, J.B.; Dandenaault, B.; Duchaine, C.; Poirier, G.G.
FEBS Lett. 302, 269-273, 1992
A/Title: Structural analysis of the putative regulatory region of the rat gene encoding
A/Reference number: S21163; MUID:92290013; PMID:1601134
A/Accession: S21163
A/Molecule type: DNA
A/Residues: 1-12 <POT>
A/Cross-references: UNIPARC:UPI0000170AA3; EMBL:X65496; NID:956847; PIDN:CAA46477.1; PIR

C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 VAKSVKSLY 13
:|:|:|
DB 1 MAEATERLY 9

RESULT 28

PH1463
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1463

R;Caenova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1463

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Cross-references: UNIPARC:UPI000017C798

A;Experimental source: cytolytic T-lymphocyte

C;Keywords: receptor; T-cell

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 SYLIG 15
:|:|:|
DB 8 TLTYFG 12

RESULT 29

PH1464
T-cell receptor beta chain (clone A3/63) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1464

R;Caenova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1464

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Cross-references: UNIPARC:UPI000017C798

A;Experimental source: cytolytic T-lymphocyte

C;Keywords: receptor; T-cell

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 SYLIG 15
:|:|:|
DB 8 TLTYFG 12

RESULT 30

PH1468
T-cell receptor beta chain - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1468; PH1465

R;Caenova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1468

A;Molecule type: mRNA

A;Residues: 1-12 <CAS1>

A;Cross-references: UNIPARC:UPI000017C7A9

A;Experimental source: cytolytic T-lymphocyte, clone A24/PER2

A;Accession: PH1465

A;Molecule type: mRNA

A;Residues: 1-12 <CAS2>

A;Cross-references: UNIPARC:UPI000017C7A9

A;Experimental source: cytolytic T-lymphocyte, clone 332/2G

C;Keywords: receptor; T-cell

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 SYLIG 15
:|:|:|
DB 8 TLTYFG 12

RESULT 31

C60529
hemocyanin 1 - green crab (fragment)

C;Species: Carcinus maenas (green crab, common shore crab)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004

C;Accession: C60529

R;Neuteboom, B.; Sierdema, S.J.; Beintema, J.J.

Comp. Biochem. Physiol. B 94, 587-592, 1989

A;Title: The relationship between N-terminal sequences and immunological characterization

A;Reference number: A60529; MUID:90151075; PMID:2620501

A;Accession: C60529

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <NEU>

A;Cross-references: UNIPROT:P83176; UNIPARC:UPI000012C375

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 5.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVK 10
|:|:|:|
DB 3 PASVSDAKK 11

RESULT 32

S47384
T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47384

R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47385

A;Accession: S47384

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: UNIPARC:UPI0000116689; EMBL:Z35704; NID:9527501; PIDN:CAA84773.1; PI

C;Keywords: T-cell receptor

Query Match 25.0%; Score 18; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
|:|:|:|
DB 2 ASSRSRAV 9

RESULT 33

B61620
 locustamyotropin IV - migratory locust
 C:Species: locusta migratoria (migratory locust)
 C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
 C/Accession: B61620
 R/Schoofers, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
 Insect Biochem. Mol. Biol. 22, 447-452, 1992
 A>Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add
 A/Reference number: A61620
 A/Accession: B61620
 A>Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <SCH>
 A/Title: KSAVMRFamide: a novel FMRFamide-related heptapeptide from the free-living nema
 A/Reference number: PC2132; MUID:94235053; PMID:8179635
 A/Accession: PC2132
 A/Molecule type: protein
 A/Residues: 1-7 <MAU>
 A/Cross-references: UNIPROT:P41874; UNIPARC:UPI000003AD32
 C/Keywords: amidated carboxyl end
 F:7/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 25.0%; Score 18; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
 Db 7 MPFS 10

RESULT 34
 NYPG14
 hypothalamic tetradecapeptide - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
 C/Accession: A01419
 R/Schlesinger, D.H.; Nally, H.D.; Linthicum, G.L.; Dupont, A.; Schally, A.V.
 submitted to the Atlas, November 1976
 A/Reference number: A01419
 A/Accession: A01419
 A/Molecule type: protein
 A/Residues: 1-14 <SCH>
 A/Cross-references: UNIPROT:P01155; UNIPARC:UPI000012CFC3
 C/Keywords: amidated carboxyl end; hypothalamus
 F:14/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 25.0%; Score 18; DB 1; Length 14;
 Best Local Similarity 55.6%; Pred. No. 6.8e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 ANSVKSLYL 14
 Db 1 ARYGRKSPYL 9

RESULT 35
 B59137
 protein PFI - golden needle mushroom (fragment)
 C:Species: Flammulina velutipes (golden needle mushroom)
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: B59137
 R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
 submitted to the Protein Sequence Database, November 1999
 A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
 A/Reference number: A59137
 A/Accession: B59137
 A/Molecule type: protein
 A/Residues: 1-15 <SKA>
 A/Cross-references: UNIPROT:Q7M4X0; UNIPARC:UPI000017CB23
 A/Experimental source: strain FV-4

Query Match 25.0%; Score 18; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 7.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSV 5

Db 9 VPMSI 13

RESULT 36
 PC2132
 FMRFamide-related heptapeptide - Panagrellus redivivus
 C:Species: Panagrellus redivivus
 C>Date: 03-May-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
 C/Accession: PC2132
 R/Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, T.G.; Thim,
 Biochem. Biophys. Res. Commun. 200, 973-980, 1994
 A/Title: KSAVMRFamide: a novel FMRFamide-related heptapeptide from the free-living nema
 A/Reference number: PC2132; MUID:94235053; PMID:8179635
 A/Accession: PC2132
 A/Molecule type: protein
 A/Residues: 1-7 <MAU>
 A/Cross-references: UNIPROT:P41874; UNIPARC:UPI000003AD32
 C/Keywords: amidated carboxyl end
 F:7/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 23.6%; Score 17; DB 2; Length 7;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYL 14
 Db 1 KSAVM 5

RESULT 37
 A13687
 caerulein-like peptide - African tree frog (Kaasina maculata)
 C:Species: Kaasina maculata
 C>Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: A13687
 R/Montecucchi, P.; Falconieri Erpamer, G.; Visser, J.
 Experientia 33, 1138-1139, 1977
 A>Title: Occurrence of Asn(2), Leu(5)-caerulein in the skin of the African frog Hylandat
 A/Reference number: A13687; MUID:77246547; PMID:891852
 A/Accession: A13687
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <MON>
 A/Cross-references: UNIPROT:Q7LZC5; UNIPARC:UPI000017668C
 C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:4/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.6%; Score 17; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YLG 15
 Db 4 YLG 6

RESULT 38
 C39745
 sphingomyelinase - Rhodococcus sp. (fragment)
 C:Species: Rhodococcus sp.
 C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
 C/Accession: C39745
 R/Ito, M.; Ikegami, Y.; Yamagata, T.
 J. Biol. Chem. 266, 7919-7926, 1991
 A>Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidases. E
 ble using these activator proteins.
 A/Reference number: A39745; MUID:91210321; PMID:1850427
 A/Accession: C39745
 A/Status: preliminary

A:Molecule type: protein
A:Residues: 1-10 <ITO>
A:Cross-references: UNIPARC:UPI000017AD7A

Query Match 23.6%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VFPSVA 6
DB 4 LPASTA 9

RESULT 39

B49164

Chromogranin-B - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C:Accession: B49164

R:Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A>Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th

A:Reference number: A49164; MUID:92063871; PMID:1954895

A:Accession: B49164

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <NIE>

A:Cross-references: UNIPARC:UPI00000E7128

A:Notes: sequence extracted from NCBI backbone (NCBIP:66370)

C:Superfamily: chromogranin B precursor

Query Match 23.6%; Score 17; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFS 4
DB 1 PFS 3

RESULT 40

PC2372

58k heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)

C:Species: Bacillus cereus

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: PC2372

R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanaka, S.

Bioest. Biotechnol. Biochem. 59, 231-235, 1995

A>Title: Identification of DNA-binding proteins changed after induction of sporulation i

A:Reference number: PC2369; MUID:95218265; PMID:7766022

A:Accession: PC2372

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <MAS>

A:Cross-references: UNIPARC:UPI000017AC8A

C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 23.6%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVK 10
DB 1 AKDIK 5

RESULT 41

S43957

Ig mu chain V region (clone 3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999

C:Accession: S43957

R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.

Nucleic Acids Res. 22, 1389-1393, 1994
A>Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43957
A:Molecule type: DNA
A:Residues: 1-12 <WAG>
A:Cross-references: UNIPARC:UPI000017C26A
C:Keywords: immunoglobulin

Query Match 23.6%; Score 17; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSV 5
DB 5 PFDV 8

RESULT 42

PH0785

T-cell receptor alpha chain (OAI1.3.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0785

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A>Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0785

A:Molecule type: mRNA

A:Residues: 1-12 <CRAS>

A:Cross-references: UNIPARC:UPI000017C781; EMBL:X60887

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LYLG 15
DB 9 LYFG 12

RESULT 43

P00696

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: P00696

R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A>Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A:Reference number: P00696

A:Accession: P00696

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <KOM>

A:Cross-references: UNIPROT:Q7M284; UNIPARC:UPI000017B0EC

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 23.6%; Score 17; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSV 5
DB 6 PFNI 9

RESULT 44

PT0263

Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0263
R:Yamada, M.; Wesselman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0263
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Cross-references: UNIPARC:UPI000017C1F0
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YLG 15
|||
Db 9 YLG 11

RESULT 45
S47356
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47356
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116676; EMBL:Z35680; NID:G527449; PIDN:CAA84749.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 9.7e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
|:|:|:
Db 3 SSTRSTDTQYL 13

RESULT 46
S47359
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47359
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47359
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116679; EMBL:Z35683; NID:G527455; PIDN:CAA84752.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
|:|:|:

Db 2 ASSRSRSY 9

RESULT 47,
S47371
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47371
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116683; EMBL:Z35696; NID:G527483; PIDN:CAA84765.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
|:|:|:
Db 2 ASSIRS 7

RESULT 48
S47373
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47373
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47373
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116671; EMBL:Z35672; NID:G527489; PIDN:CAA84741.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
|:|:|:
Db 2 ASSIRS 7

RESULT 49
S47380
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47380
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47380
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116672; EMBL:Z35673; NID:G527511; PIDN:CAA84742.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 AKSVKS 11
| : : : |
Db 2 ASSIRS 7

RESULT 50
S47390
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47390
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
A:Reference number: S47355
A:Accession: S47390
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116688; EMBL:Z35703; NID:G527459; PIDN:CAA84772.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
| : : : |
Db 2 ASSIRS 7

RESULT 51
S47392
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47392
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
A:Reference number: S47355
A:Accession: S47392
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116690; EMBL:Z35713; NID:G527521; PIDN:CAA84782.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
| : : : |
Db 2 ASSIRS 7

RESULT 52
S20578
ribosomal protein L36 - *Cryptomonas* sp. chloroplast (fragment)
C:Species: Chloroplast *Cryptomonas* sp.
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S20578
R:Douglas, S.E.
FEBS Lett. 298, 93-96, 1992
A:Title: A secY homologue is found in the plastid genome of *Cryptomonas* Ph.
A:Reference number: S20577; MUID:92183838; PMID:1544427
A:Accession: S20578
A:Molecule type: DNA
A:Residues: 1-13 <DOU>

A:Cross-references: UNIPROT:P28528; UNIPARC:UPI000017AED5; EMBL:X62348; NID:G11300; PID
A>Note: the source is designated as *Cryptomonas* ph
C:Genetics:
A:Gene: rpl36
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 VAKSVKSL 12
| : : : |
Db 3 VVSSIGSL 10

RESULT 53
JZVHPI
crabrolin - European hornet
C:Species: *Vespa crabro* (European hornet)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C:Accession: A01781
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,
A:Reference number: A92441; MUID:84289390; PMID:6206053
A:Accession: A01781
A:Molecule type: protein
A:Residues: 1-13 <ARG>
A:Cross-references: UNIPROT:P01518; UNIPARC:UPI00001283DB
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
C:Keywords: amidated carboxyl end; venom
F:13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 9.7e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSL 12
: : : : :
Db 2 LPLIRKIVTAL 13

RESULT 54
QMWHP2
mastoparan C - European hornet
C:Species: *Vespa crabro* (European hornet)
C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 09-Jul-2004
C:Accession: A01779
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,
A:Reference number: A92441; MUID:84289390; PMID:6206053
A:Accession: A01779
A:Molecule type: protein
A:Residues: 1-14 <ARG>
A:Cross-references: UNIPROT:P01516; UNIPARC:UPI000012EBD3
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end; venom
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 23.6%; Score 17; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSV 9
: : : : :
Db 8 AVAKKI 13

RESULT 55
PA0015

seed storage protein 12S 2 - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
C/Accession: PA0015
R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A/Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A/Reference number: PA0001
A/Accession: PA0015
A/Molecule type: protein
A/Residues: 1-14 <K&M>
A/Cross-references: UNIPARC:UPI000017B010
A/Experimental source: seed
C/Keywords: pyroglutamic acid; seed; storage protein
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 23.6%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YLG 15
DB 3 YLG 5

RESULT 56
PT0223
Ig heavy chain CDR3 region (clone 1-88B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0223
R/Yamada, M.; Maeser, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0223
A/Molecule type: DNA
A/Residues: 1-14 <Y&M>
A/Cross-references: UNIPARC:UPI000017C1D5
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 23.6%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPP 3
DB 5 VPP 7

RESULT 57
S36678
dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydroxyacyl-CoA hydratase (EC 4.2.1.11)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C/Accession: S36678
R/Chen, N.; Crane, D.I.
Biochem. J. 283, 605-610, 1992
A/Title: Induction of the major integral membrane protein of mouse liver peroxisomes by
A/Reference number: S21285; MUID:92246895; PMID:1575703
A/Accession: S36678
A/Molecule type: protein
A/Residues: 1-14 <C&H>
A/Cross-references: UNIPROT:Q7M0E0; UNIPARC:UPI000017C652
A/Experimental source: liver
C/Function:
A/Pathway: fatty acid beta-oxidation
C/Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 23.6%; Score 17; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFPSVA 6
DB 7 PFPSVA 11

RESULT 58
LFECP
phe operon leader peptide - Escherichia coli (strain K-12)
N/Alternate names: attenuator peptide
C/Species: Escherichia coli
C/Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C/Accession: A03593; B36494; A65038
R/Zurawski, G.; Brown, K.; Killingley, D.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978
A/Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli
A/Reference number: A03593; MUID:79033820; PMID:360214
A/Accession: A03593
A/Molecule type: DNA
A/Residues: 1-15 <Z&R>
A/Cross-references: UNIPROT:P03057; UNIPARC:UPI000012E851; GB:V00314; GB:J01658; MID:94
R/Gavini, N.; Davidson, B.E.
J. Biol. Chem. 265, 21532-21535, 1990
A/Title: Pheo mutants of Escherichia coli have a defective pheA attenuator.
A/Reference number: A36494; MUID:91072346; PMID:2254312
A/Accession: B36494
A/Molecule type: DNA
A/Residues: 1-15 <G&V>
A/Cross-references: UNIPARC:UPI000012E851; GB:M58024; GB:J05694; MID:9147178; PIDN:AAA6
R/Batner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65038
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-15 <B&A>
A/Cross-references: UNIPARC:UPI000012E851; GB:AE00346; GB:U00096; MID:92367141; PIDN:AA6
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: pheL; pheA
A/Map position: 56 min
C/Superfamily: pheA leader peptide

Query Match 23.6%; Score 17; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPPSVA 6
DB 4 IPPFPA 9

RESULT 59
PH0784
T-cell receptor alpha chain (PI) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0784
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0784
A/Molecule type: mRNA
A/Residues: 1-15 <C&S>
A/Cross-references: UNIPARC:UPI000017C76B; EMBL:X60885
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 LYLIG 15
|||
Db 12 LYFG 15

RESULT 60
PH0797
T-cell receptor alpha chain (PF2.10.1 V-alpha-3.AR5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0797
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0797
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI000017C780; EMBL:X60903
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 25.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYLIG 15
|||
Db 4 SITGNTRKLIIG 15

RESULT 61
PH0750
T-cell receptor beta chain (C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0750
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0750
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI0000115FA9; EMBL:X06841
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LYLIG 15
|||
Db 12 LYFG 15

RESULT 62
PH0751
T-cell receptor beta chain (F12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0751
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0751
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI0000115FA9; EMBL:X60843; NID:g50931; PTDN:CAA43235.1; PIC
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LYLIG 15
|||
Db 12 LYFG 15

RESULT 63
S77987
cytochrome-c oxidase (EC 1.9.3.1) chain vic.2 - bigeye tuna (fragments)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: S77987
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77987
A:Molecule type: protein
A:Residues: 1-8;9-15 <ARN>
A:Cross-references: UNIPROT:P80978; UNIPARC:UPI000017BF73; UNIPARC:UPI000017BF74
A:Experimental source: heart
C:Genetics:
A:Genome: nuclear
A:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 VAKSVKSLYLIG 13
|||
Db 6 VAKKPMSDY 14

RESULT 64
A41436
alpha-macroglobulin - green sea turtle (fragment)
C:Species: Chelonia mydas (green sea turtle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41436
R:Osada, T.; Sasaki, T.; Imai, A.
J. Biochem. 103, 212-217, 1988
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin o
A:Reference number: A41436; MUID:86227890; PMID:2453503
A:Accession: A41436
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OSA>
A:Cross-references: UNIPROT:Q7LZ35; UNIPARC:UPI000017BFB3

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPF 3
|||
Db 10 VPF 12

RESULT 65
A61140
sperm acrosomal protein - spoonworm (Urechis caupo) (fragment)

C/Species: Urechis caupo
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-Apr-1994
C/Accession: A61140
R/Gould, M.C.; Stephano, J.L.
Dev. Biol. 146, 509-518, 1991
A/Title: Peptides from sperm acrosomal protein that initiate egg development.
A/Reference number: A61140; MUID:91323672; PMID:1864468
A/Accession: A61140
A/Molecule type: protein
A/Residues: 1-6 <GOU>
A/Cross-references: UNIPARC:UPI000017BD8D

Query Match 22.2%; Score 16; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 VAKSVK 10
|||
Db 1 VAKKPK 6

RESULT 66

C24180
Fibrinogen beta chain - Japanese macaque (fragment)
N/Contains: fibrinopeptide B
C/Species: Macaca fuscata (Japanese macaque)
C/Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C/Accession: C24180
R/Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A/Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E. venosus) and baboons.
A/Reference number: A91990; MUID:85289140; PMID:3928610
A/Accession: C24180
A/Molecule type: protein
A/Residues: 1-9 <NAK>
A/Cross-references: UNIPROT:P19345; UNIPARC:UPI000012A77B
C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 22.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLK 15
|||
Db 3 ESLFSG 8

RESULT 67

PC7073
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C/Accession: PC7073
R/Tsugita, A.; Kakawami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A/Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of
A/Reference number: PC7072
A/Accession: PC7073
A/Molecule type: protein
A/Residues: 1-9 <TSU>
A/Cross-references: UNIPROT:Q9CVK7; UNIPARC:UPI000017CDE7
A/Keywords: brain; core protein; oxidoreductase

Query Match 22.2%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 VAKSVK 10
|||
Db 4 VAKPKV 9

RESULT 68

PC4442
Cytochrome c553 - Desulfovibrio desulfuricans (fragment)
C/Species: Desulfovibrio desulfuricans
C/Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Jul-2004
C/Accession: PC4442
R/Abbert, C.; Leroy, G.; Bianco, P.; Forest, E.; Bruschi, M.; Dolla, A.
Biochem. Biophys. Res. Commun. 242, 213-218, 1998
A/Title: Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.
A/Reference number: PC4442; MUID:98102811; PMID:9439638
A/Accession: PC4442
A/Molecule type: protein
A/Residues: 1-10 <AUB>
A/Cross-references: UNIPROT:Q7M0M6; UNIPARC:UPI000017AB62
A/Experimental source: strain G201
C/Comment: This protein is involved in the formate reduction pathway.

Query Match 22.2%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 AKSVKSLY 13
|||
Db 1 AEDGASLY 8

RESULT 69

P00029
33K protein 3218 - rice (strain Nohonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C/Accession: P00029
R/Tsugita, A.; Miyake, N.
Submitted to JIPID, April 1993
A/Reference number: PS0208
A/Accession: P00029
A/Molecule type: protein
A/Residues: 1-11 <TSU>
A/Cross-references: UNIPARC:UPI000017B0FE
A/Experimental source: bran
C/Comment: molecular weight 33K, pI 6.0.

Query Match 22.2%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PFSV 5
|||
Db 6 PFXI 9

RESULT 70

S58244
pyrrolquinoline quinone synthase C - Pseudomonas fluorescens (fragment)
C/Species: Pseudomonas fluorescens
C/Date: 11-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58244
R/Schneider, U.; Keel, C.; Defago, G.; Haas, D.
Submitted to the EMBL Data Library, May 1995
A/Description: Tn5-directed cloning of pqd genes from Pseudomonas fluorescens CHA0: the
A/Reference number: S58239
A/Accession: S58244
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-11 <SCH>
A/Cross-references: UNIPROT:P55173; UNIPARC:UPI000013130; EMBL:X87299; NID:9929799; PI

Query Match 22.2%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PFSVAK 7
|||

Db 5 PLUSAE 10

RESULT 71

H64082

hypothetical protein BH3464 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: H64082

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H64082

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <STO>

A:Cross-references: UNIPROT:Q9K744; UNIPARC:UP100000C41E3; GB:AP001518; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH3464

Query Match 22.2%; Score 16; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 1.2e+04;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 VKSLVYG 15

Db 3 VKELSLG 9

RESULT 72

S00616

parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae

N:Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C:Species: *Bacillus thuringiensis*

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004

C:Accession: S00616

R:Chetukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 232, 249-251, 1988

A:Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two delta-endotox

A:Reference number: S00615

A:Accession: S00616

A:Molecule type: protein

A:Residues: 1-11 <CHE>

A:Cross-references: UNIPROT:Q7M54; UNIPARC:UP100001781A1

C:Comment: This toxin is effective against the larvae of *Galleria mellonella* (greater wax

C:Keywords: delta-endotoxin

Query Match 22.2%; Score 16; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVA 6

Db 7 PYSQA 11

RESULT 73

LFECPE

pyrE leader peptide - *Escherichia coli*

C:Species: *Escherichia coli*

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A30400; A05110; Q00495

R:Poulsen, P.; Bonekamp, F.; Jensen, K.F.

EMBO J. 3, 1783-1790, 1984

A:Title: Structure of the *Escherichia coli* pyrE operon and control of pyrE expression by

A:Reference number: A30400; MUID:85003588; PMID:6207018

A:Accession: A30400

A:Molecule type: DNA

A:Residues: 1-12 <POU>

A:Cross-references: UNIPROT:P17776; UNIPARC:UP1000013C2E1

R:Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.

Eur. J. Biochem. 135, 223-229, 1983

A:Title: Nucleotide sequence of the *Escherichia coli* pyrE gene and of the DNA in front

A:Reference number: A05110; MUID:83287414; PMID:6349999

A:Accession: A05110

A:Molecule type: DNA

A:Residues: 1-12 <POU>

A:Cross-references: UNIPARC:UP1000013C2E1

C:Genetics:

A:Gene: pyrE-LP

C:Superfamily: pyrE leader peptide

Query Match 22.2%; Score 16; DB 1; Length 12;

Best Local Similarity 37.5%; Pred. No. 1.4e+04;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 FSVAKSVK 10

Db 5 FVCRKVR 12

RESULT 74

A28856

fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment)

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 31-Oct-1997

C:Accession: A28856

R:Hamappel, E.; MacGregor, J.S.; Davoust, S.; Horecker, B.L.

Arch. Biochem. Biophys. 214, 293-298, 1982

A:Title: Limited proteolysis of liver and muscle aldolases: effects of subtilisin, cathe

A:Reference number: A28856; MUID:82205113; PMID:7044315

A:Accession: A28856

A:Molecule type: protein

A:Residues: 1-12 <HAN>

A:Cross-references: UNIPARC:UP10000175FP2

C:Superfamily: fructose-bisphosphate aldolase

C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; pen

Query Match 22.2%; Score 16; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 1.4e+04;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVKSLY 13

Db 1 STQSLF 6

RESULT 75

S47362

T-cell antigen receptor VJ junction beta chain - human

C:Species: *Homo sapiens* (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47362

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A:Reference number: S47355

A:Accession: S47362

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UP1000011667E; EMBL:Z35688; NID:gs27465; PIDN:CAA84757.1; PI

C:Keywords: T-cell receptor

Query Match 22.2%; Score 16; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.5e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKS 11

Db 2 ASVSVS 7

RESULT 76

S47368

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47368

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47368

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UPI0000116681; EMBL:Z35693; NID:9527477; PIDN:CAA84762.1; PI

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 22.2%; Score 16; DB 2; Length 13;

Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13

DB 2 ASSTRGAY 9

RESULT 77

S47400

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47400

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47400

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UPI0000116675; EMBL:Z35678; NID:9527535; PIDN:CAA84747.1; PI

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 22.2%; Score 16; DB 2; Length 13;

Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 SVAKSVKSLY 13

DB 4 SVALATEAF 13

RESULT 78

A60336

outer membrane protein OmpA homolog - Actinobacillus actinomycetemcomitans (fragment)

C:Species: Actinobacillus actinomycetemcomitans

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 31-Dec-2004

C:Accession: A60336

R:Wilson, M.E.

Immun. 59, 2505-2507, 1991

A:Title: The heat-modifiable outer membrane protein of Actinobacillus actinomycetemcomit

A:Reference number: A60336; PMID:9126765; PMID:2050416

A:Accession: A60336

A:Molecule type: protein

A:Residues: 1-13 <WIL>

A:Cross-references: UNIPROT:Q9S5U9; UNIPROT:O51841; UNIPARC:UPI00001780B0

C:Keywords: membrane protein

QY 6 AKSVKSLYLG 15

DB 1 APQANTEYAG 10

RESULT 79

S13864

methyl coenzyme M reductase (EC 1.8.-.-) II alpha chain - Methanobacterium thermoautotro

C:Species: Methanobacterium thermoautotrophicum

C:Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 30-Oct-1998

C:Accession: S13864

R:Roepert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.

Eur. J. Biochem. 194, 871-877, 1990

A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium cher

A:Reference number: S13864; PMID:9109370; PMID:2269306

A:Accession: S13864

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Cross-references: UNIPARC:UPI000012EDDF

A:Experimental source: strain Marburg

C:Keywords: methanogenesis; oxidoreductase

Query Match

Best Local Similarity 22.2%; Score 16; DB 2; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYL 14

DB 4 KKLFL 8

RESULT 80

S11074

alcohol dehydrogenase (EC 1.1.1.1) - Baltic cod (fragments)

C:Species: Gadus morhua callarias (Baltic cod)

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Jan-1997

C:Accession: S11074

R:Begstad, B.; Bastoni, M.; Danielsson, O.; Persson, B.; Cedertund, E.; Kaiser, R.; Ho

FBS Lett. 269, 194-196, 1990

A:Title: Fast atom bombardment mass spectrometry and chemical analysis in determination

A:Reference number: S11074; PMID:90353571; PMID:2387402

A:Accession: S11074

A:Molecule type: protein

A:Residues: 1-5,6-14 <RGE>

A:Cross-references: UNIPARC:UPI000017BF65; UNIPARC:UPI000017BF66

C:Keywords: acetylated amino end; alcohol metabolism; NAD; oxidoreductase

F;1/Modified site: acetylated amino end (Ala) #status experimental

Query Match

Best Local Similarity 22.2%; Score 16; DB 2; Length 14;

Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12

DB 2 TWGKCIRTV 10

Search completed: July 12, 2006, 05:39:44

Job time : 46 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:30:49 ; Search time 293 Seconds
(without alignments)
47.356 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSAKSVKSLYLIG_15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 800 summaries

Database :

1: uniprot_7.2:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	34.7	14	2 Q7M4W9	FLAVE
2	24	33.3	15	2 Q798U8	STROK
3	23	31.9	10	1 MDAR2	SOYBN
4	23	31.9	14	1 CRBL	VESOR
5	23	31.9	14	2 Q5G1T6	ASPL
6	23	31.9	14	2 Q7M487	ANDAU
7	23	31.9	14	2 Q3TU57	MOUSE
8	22	30.6	8	2 P82858	GBASI
9	22	30.6	8	2 P92386	HORWA
10	22	30.6	14	2 Q6E0X9	YEAST
11	22	30.6	15	1 ASPI	LACSN
12	22	30.6	15	2 P83331	STRTR
13	21	29.2	8	2 P92211	AGRCR
14	21	29.2	8	2 P92215	9POL
15	21	29.2	8	2 P92222	BROIN
16	21	29.2	8	2 P92227	CRIDE
17	21	29.2	8	2 P92373	haynaldia v
18	21	29.2	8	2 P92382	9POL
19	21	29.2	8	2 P92384	9POL
20	21	29.2	8	2 P92388	9POL
21	21	29.2	8	2 P92391	HERPI
22	21	29.2	8	2 P92394	HORVU
23	21	29.2	8	2 P92404	LOPEL
24	21	29.2	8	2 P92422	PSAPR
25	21	29.2	8	2 P92426	PSEBP
26	21	29.2	8	2 P92428	9POL
27	21	29.2	8	2 P92431	AEGRF
28	21	29.2	8	2 P92441	THRE
29	21	29.2	8	2 P92443	TABCM
30	21	29.2	8	2 P93955	FESSE
31	21	29.2	8	2 P93957	FESSE

32	21	29.2	8	2 P93959	9POL
33	21	29.2	8	2 P93961	PSART
34	21	29.2	8	2 P93963	PSART
35	21	29.2	8	2 P93965	SECT
36	21	29.2	8	2 P93966	AEGBP
37	21	29.2	8	2 P93970	9POL
38	21	29.2	8	2 P93973	EREDL
39	21	29.2	8	2 P93981	9POL
40	21	29.2	8	2 P93985	AEGBM
41	21	29.2	8	2 P93992	AUSBE
42	21	29.2	9	2 Q5EFY1	9BRIO
43	21	29.2	9	2 Q5EFY7	9BRIO
44	21	29.2	9	2 Q5EFZ0	9BRIO
45	21	29.2	10	2 Q3YLM8	STRAB
46	21	29.2	12	2 Q31851	ARATH
47	21	29.2	14	2 Q714T5	9CRIP
48	21	29.2	14	2 Q85662	REOVJ
49	21	29.2	15	2 Q9UC22	HUMAN
50	21	29.2	15	2 Q4X416	PLACH
51	21	29.2	15	2 Q714T8	9FLOR
52	20	27.8	10	2 Q755J5	NEUR
53	20	27.8	10	2 P83161	ANASL
54	20	27.8	11	2 Q53VR5	MOUSE
55	20	27.8	11	2 Q86866	9VIRU
56	20	27.8	11	2 Q86868	9VIRU
57	20	27.8	12	1 HCVB	MEGCR
58	20	27.8	12	2 Q945C3	CRYCO
59	20	27.8	12	2 Q6VSD4	9LAKR
60	20	27.8	13	1 UPE71	LITEM
61	20	27.8	13	1 Q14461	HUMAN
62	20	27.8	14	1 BRK3	RANNT
63	20	27.8	14	1 HCVJ	MEGCR
64	20	27.8	14	2 Q96050	HUMAN
65	20	27.8	15	2 Q38Z05	LACCS
66	19	26.4	8	2 Q70Y88	9LAMI
67	19	26.4	9	2 Q6UQJ3	MACCV
68	19	26.4	9	2 Q6U7P3	RALBU
69	19	26.4	10	2 Q47651	ECOLI
70	19	26.4	11	2 Q9UCP2	HUMAN
71	19	26.4	11	2 Q59AK1	9COLS
72	19	26.4	12	2 Q5U1X7	9FLOR
73	19	26.4	12	2 Q6PAJ9	MOUSE
74	19	26.4	13	1 DAH11	LITDA
75	19	26.4	13	1 SAHH1	POPEU
76	19	26.4	13	1 SAHH2	POPEU
77	19	26.4	13	2 Q97122	TOXKO
78	19	26.4	13	2 Q9U7D6	NEOCA
79	19	26.4	13	2 Q50038	MYCLE
80	19	26.4	14	2 Q4XAS9	PLACH
81	19	26.4	14	2 Q5U7U8	9FLOR
82	19	26.4	14	2 Q9R506	BURCE
83	19	26.4	14	2 Q78EC9	RAT
84	19	26.4	15	1 CWP14	THAVU
85	19	26.4	15	1 CMPI6	TOBAC
86	19	26.4	15	2 Q5U1X3	9FLOR
87	18	25.7	15	2 Q571P1	AERPU
88	18	25.0	10	1 ANGT	CHICK
89	18	25.0	10	1 ANGT	COTUA
90	18	25.0	10	2 Q7WUG1	PSEFL
91	18	25.0	11	2 Q2KKK1	9BRIO
92	18	25.0	11	2 Q707P1	RAT
93	18	25.0	11	2 Q77893	ORENI
94	18	25.0	12	1 HCVI	CARMA
95	18	25.0	12	2 Q6KEF1	HUMAN
96	18	25.0	12	2 Q7KYL7	HUMAN
97	18	25.0	12	2 Q7RNA6	PLAYO
98	18	25.0	12	2 Q3ZBX8	BOVIN
99	18	25.0	12	2 Q8SXB1	BRP69
100	18	25.0	12	2 Q4KUI2	9FLOR
101	18	25.0	12	2 Q4KUI8	9FLOR
102	18	25.0	12	2 Q4KUI8	9FLOR
103	18	25.0	12	2 Q4KUI4	9FLOR
104	18	25.0	12	2 Q4KUI0	9FLOR

P93959	hordeum ere
P93961	psathyrosta
P93963	psathyrosta
P93965	secale berr
P93966	aequallops sp
P93970	eremopyrum
P93973	eremopyrum
P93981	aequallops co
P93985	aequallops co
P93992	australiopyr
Q5EFY1	polycichum
Q5EFY7	cedipodium
Q5EFZ0	buxbaumia a
Q3YLM8	strix aluco
Q31851	arabidopsis
Q714T5	rhodomonas
Q85662	reovirus ty
Q9UC22	homo sapien
Q4X416	plasmidium
Q714T8	masid.alfus
Q755J5	neurospora
P83161	anabena. sp
Q53VR5	mus muscicu
Q86866	lymphocyti
Q86868	lymphocyti
Q10584	megathura c
Q945C3	cryptocodi
Q6VSD4	thalassoma
P82050	litoria ewi
Q14461	homo sapien
Q71253	rana nigrom
Q10583	megathura c
Q96050	homo sapien
Q38Z05	lactobacilli
Q70Y88	placostoma
Q6UQJ3	macaca mula
Q6U7P3	ralesonia e
Q47651	escherichia
Q9UCP2	homo sapien
Q59AK1	cicindela (
Q5U1X7	gracilaria
Q6PAJ9	mus muscicu
DAH11	litoria dah
SAHH1	populus eup
SAHH2	populus eup
Q97122	toxoplasma
Q9U7D6	neopora ca
Q50038	mycobacteri
Q4XAS9	plasmidium
Q5U7U8	gracilaria
Q9R506	burholderi
Q78EC9	rattus norv
P80773	phaseolus v
P80793	nicotiana t
Q5U1X3	gracilaria
Q571P1	aeromonas p
P67865	gallus gall
P67866	colurnix co
Q7WUG1	pseudomonas
Q2KKK1	fissidens s
Q707P1	rattus norv
Q77893	oreochromis
P83176	carcinus ma
Q6KEF1	homo sapien
Q7KYL7	homo sapien
Q7RNA6	plasmidium
Q3ZBX8	bos taurus
Q8SXB1	bacterioph
Q4KUI2	graceloupi
Q4KUI8	graceloupi
Q4KUI8	graceloupi
Q4KUI4	graceloupi
Q4KUI0	graceloupi

105	18	25.0	12	2	04KUK4_9FLOR	Q4kuk4	grateloupia	178	17	23.6	12	2	Q6VSE8_9LABR	O6vee8	thalassoma
106	18	25.0	12	2	Q8SEB8_9FLOR	Q8seb8	grateloupia	179	17	23.6	12	2	O6VSE9_9LABR	O6vef1	thalassoma
107	18	25.0	12	2	Q8SEB9_9FLOR	Q8seb9	grateloupia	180	17	23.6	12	2	O6VSP1_9LABR	O6vef2	thalassoma
108	18	25.0	13	1	CRBL_VESLE	P17235	vespula lew	181	17	23.6	12	2	O6VSP2_9LABR	O6vef3	thalassoma
109	18	25.0	13	1	DAH12_LITDA	P84263	littoria dan	182	17	23.6	12	2	O6VSP3_9LABR	O6vef4	thalassoma
110	18	25.0	13	1	LMT4_LOCM1	P41490	locustia mig	183	17	23.6	12	2	O6VSP4_9LABR	O6vef5	thalassoma
111	18	25.0	13	1	VG16_BACSU	P80867	bacillus su	184	17	23.6	12	2	O6VSP5_9LABR	O6vef6	thalassoma
112	18	25.0	13	2	Q8WKG0_HUMAN	O8wkg0	homo sapien	185	17	23.6	12	2	O6VSP6_GOMVA	O6vef6	gomphosus v
113	18	25.0	13	2	Q6GEU5_STREBO	O6geu5	streplococc	186	17	23.6	12	2	O5AXH6_9HTV1	O58xh6	human
114	18	25.0	13	2	O6LCB1_RAT	O6lcb1	rattus norv	187	17	23.6	12	2	O5AXH8_9HTV1	O58xh8	human
115	18	25.0	14	1	FEET_TOBAC	P82150	nicotiana t	188	17	23.6	12	2	O58X10_9HTV1	O58x10	human
116	18	25.0	14	1	HY14_PYG	P01155	sus scrofa	189	17	23.6	12	2	O5ETV0_9HTV1	O5etv0	human
117	18	25.0	14	2	Q4XJS2_PLACH	Q4xjs2	plasmodium	190	17	23.6	12	2	O5ETV4_9HTV1	O5etv4	human
118	18	25.0	14	2	Q69ES5_STREBO	Q69es5	streplococc	191	17	23.6	12	2	O5ETV6_9HTV1	O5etv6	human
119	18	25.0	15	1	HSP11_BINPS	P81083	pinus pins	192	17	23.6	12	2	O5ETV8_9HTV1	O5etv8	human
120	18	25.0	15	2	Q7M4X0_FLAWE	Q7m4x0	flammulina	193	17	23.6	12	2	O5ERT0_9HTV1	O5ert0	human
121	18	25.0	15	2	Q95OP6_9PUNG	Q95op6	rhizophydlu	194	17	23.6	12	2	O5ERT2_9HTV1	O5ert2	human
122	18	25.0	15	2	Q71GVO_9HME	Q71gvo	andrena teg	195	17	23.6	12	2	O5EU04_9HTV1	O5eu04	human
123	18	25.0	15	2	Q9TRM3_BOVIN	Q9trm3	bos taurus	196	17	23.6	12	2	O5EU06_9HTV1	O5eu06	human
124	18	25.0	15	2	Q9TRM8_PIG	Q9trm8	sus scrofa	197	17	23.6	12	2	O5EU08_9HTV1	O5eu08	human
125	18	25.0	15	2	Q4GXZ9_ECOLI	Q4gxz9	escherichia	198	17	23.6	12	2	O5EU14_9HTV1	O5eu14	human
126	18	25.0	15	2	Q5DAR7_9CYAN	Q5dar7	osclillatori	199	17	23.6	12	2	O5EU16_9HTV1	O5eu16	human
127	18	25.0	15	2	Q9OZC9_MOUSE	Q9ozc9	mus musculi	200	17	23.6	12	2	O5EU18_9HTV1	O5eu18	human
128	17	24.3	14	1	MAST_ANTPM	P0C222	anterlychni	201	17	23.6	12	2	O5EU26_9HTV1	O5eu26	human
129	17	23.6	7	1	PAR3_HABCO	P81298	haemophilus	202	17	23.6	12	2	O5EU28_9HTV1	O5eu28	human
130	17	23.6	7	1	PAR3_PANRE	P41874	panagrellus	203	17	23.6	12	2	O5EU30_9HTV1	O5eu30	human
131	17	23.6	7	1	UC24_MAIZE	P80630	zea mays (m	204	17	23.6	12	2	O5EU32_9HTV1	O5eu32	human
132	17	23.6	8	1	PPK3_PERAM	P82618	periplaneta	205	17	23.6	12	2	O5EU34_9HTV1	O5eu34	human
133	17	23.6	8	2	Q9XNP8_BOOMI	Q9xnp8	boophilus m	206	17	23.6	12	2	O5EU36_9HTV1	O5eu36	human
134	17	23.6	9	1	JELL3_APIME	P84759	apis mellif	207	17	23.6	12	2	O5EU38_9HTV1	O5eu38	human
135	17	23.6	9	2	Q4YEF1_PLABE	Q4yef1	plasmodium	208	17	23.6	13	1	CRBL_ICASP	CRBL_ICASP	veespa crabr
136	17	23.6	9	2	Q3YAP7_MACMU	Q3yap7	macaca mula	209	17	23.6	13	1	O53S92_HUMAN	O53s92	homo sapien
137	17	23.6	9	2	Q35953_MOUSE	Q35953	mus musculi	210	17	23.6	13	2	O53S92_HUMAN	O53s92	homo sapien
138	17	23.6	9	2	Q7ZP19_9HTV1	Q7zpj19	human immun	211	17	23.6	13	2	O53S92_HUMAN	O53s92	homo sapien
139	17	23.6	9	2	Q7ZPJ3_9HTV1	Q7zpj3	human immun	212	17	23.6	14	1	MAST_VESCR	MAST_VESCR	veespa crabr
140	17	23.6	9	2	Q7ZPJ3_9HTV1	Q7zpj3	human immun	213	17	23.6	14	2	O6LCK3_HUMAN	O6lck3	homo sapien
141	17	23.6	9	2	Q7ZPJ5_9HTV1	Q7zpj5	human immun	214	17	23.6	14	2	O81WS6_HUMAN	O81ws6	homo sapien
142	17	23.6	9	2	Q7ZPJ7_9HTV1	Q7zpj7	human immun	215	17	23.6	14	2	O4X3A3_PLACH	O4x3a3	plasmodium
143	17	23.6	9	2	Q7ZPK1_9HTV1	Q7zpk1	human immun	216	17	23.6	14	2	O4Y7R1_PLACH	O4y7r1	plasmodium
144	17	23.6	10	1	ANOP_ANOSM	P0C005	anopliis sa	217	17	23.6	14	2	O4Y9M8_PLABE	O4y9m8	plasmodium
145	17	23.6	10	1	RIP_LUPAC	P84530	luffa acuta	218	17	23.6	14	2	O71GX0_9HME	O71gx0	andrena zef
146	17	23.6	10	2	O5O843_METVO	O5o843	methanococc	219	17	23.6	14	2	O311U6_HYLLA	O311u6	hylobates l
147	17	23.6	10	2	O5R2U3_HUMAN	O5r2u3	homo sapien	220	17	23.6	14	2	O9XJN4_9VIRU	O9xjn4	bacterioph
148	17	23.6	10	2	O4YFM5_PLABE	Q5r2u3	homo sapien	221	17	23.6	14	2	O9WRF6_9POAL	O9wrf6	hordcum mur
149	17	23.6	10	2	Q71UL3_HALRU	Q71ul3	halioris ru	222	17	23.6	14	2	O5FAN5_CAMLA	O5fan5	campylobact
150	17	23.6	10	2	Q3YLS0_STRAB	Q3yls0	strix aluco	223	17	23.6	14	2	OTM0B0_MOUSE	OTm0b0	mus musculi
151	17	23.6	10	2	O7LZC5_KASMA	O7lzc5	kassina mac	224	17	23.6	15	1	CPM11_PHYVU	CPM11_PHYVU	phaeocyt. v
152	17	23.6	11	2	Q9TOR6_BPYU	Q9tor6	bacterioph	225	17	23.6	15	1	CR6C2_THUOB	CR6c2_THUOB	thunnus ooe
153	17	23.6	11	2	Q9OVH3_9MORI	Q9gvh3	ractus sp.	226	17	23.6	15	1	LPE_ECOLI	LPE_ECOLI	escherichia
154	17	23.6	11	2	Q86864_9VIRU	Q86864	lymphocytic	227	17	23.6	15	2	Q4W671_LEMED	Q4w671	lentimula e
155	17	23.6	11	2	UKA2_HUMAN	P31144	homo sapien	228	17	23.6	15	2	O71A41_HUMAN	O71a41	homo sapien
156	17	23.6	12	2	Q7RH69_PLAYO	Q7rh69	plasmodium	229	17	23.6	15	2	O9BXO0_HUMAN	O9bxo0	homo sapien
157	17	23.6	12	2	Q6JDM4_CANFA	Q6jdm4	canis famli	230	17	23.6	15	2	O9WRE_RAPTH	O9wre	rapana thom
158	17	23.6	12	2	O4KUK6_9FLOR	Q4kuk6	grateloupia	231	17	23.6	15	2	O6QUD5_ECOLI	O6qud5	escherichia
159	17	23.6	12	2	Q7M284_ORYSA	Q7m284	oryza sativ	232	17	23.6	15	2	O9R4T2_BACIN	O9r4t2	bacillus in
160	17	23.6	12	2	Q8SEB7_9FLOR	Q8seb7	grateloupia	233	17	23.6	15	2	O2MAF1_ECOLI	O2maf1	escherichia
161	17	23.6	12	2	Q35868_MOUSE	Q35868	mus musculi	234	17	23.6	15	2	O3TXZ8_MOUSE	O3txz8	mus musculi
162	17	23.6	12	2	Q6VSD1_9LABR	Q6vsd1	thalassoma	235	17	23.6	15	2	O7LZ35_CHEMY	O7l235	chelonita my
163	17	23.6	12	2	Q6VSD2_9LABR	Q6vsd2	thalassoma	236	17	23.6	15	2	Q9PXXH_9PELA	Q9pxxh	human t-lym
164	17	23.6	12	2	Q6VSD3_9LABR	Q6vds3	thalassoma	237	17	23.6	15	2	P92219_9POAL	P92219	australopyr
165	17	23.6	12	2	Q6VSD5_9LABR	Q6vds5	thalassoma	238	17	23.6	16	2	O6LID23_MOUSE	O6lid23	mus musculi
166	17	23.6	12	2	Q6VSD6_9LABR	Q6vds6	thalassoma	239	17	23.6	16	2	CB22_SPIOI	CB22_SPIOI	spinaecia ol
167	17	23.6	12	2	Q6VSD7_9LABR	Q6vds7	thalassoma	240	17	23.6	16	2	O21BD5_HUMAN	O21bd5	macaca fusc
168	17	23.6	12	2	Q6VSD8_9LABR	Q6vds8	thalassoma	241	17	23.6	16	2	O2PCQ4_9PABA	O2pcq4	homo sapien
169	17	23.6	12	2	Q6VSD9_9LABR	Q6vds9	thalassoma	242	17	23.6	16	2	Q9R7B8_ECOLI	Q9r7b8	ratia spic
170	17	23.6	12	2	Q6VSE0_9LABR	O6vee0	thalassoma	243	17	23.6	16	2	CWP26_LYCOS	CWP26_LYCOS	lycopersico
171	17	23.6	12	2	Q6VSE2_9LABR	O6vee2	thalassoma	244	17	23.6	16	2	GS09_BACSU	GS09_BACSU	bacillus su
172	17	23.6	12	2	Q6VSE3_9LABR	O6vee3	thalassoma	245	17	23.6	16	2	P82217_BOMMO	P82217	bombyx mori
173	17	23.6	12	2	Q6VSE4_9LABR	O6vee4	thalassoma	246	17	23.6	16	2	O2KKK2_PERYO	O2kkk2	polytrichad
174	17	23.6	12	2	Q6VSE5_9LABR	O6vee5	thalassoma	247	17	23.6	16	2	O6YBH4_STRPN	O6ybh4	streplococc
175	17	23.6	12	2	Q6VSE6_9LABR	O6vee6	thalassoma	248	17	23.6	16	2			
176	17	23.6	12	2	Q6VSE7_9LABR	O6vee7	thalassoma	249	17	23.6	16	2			
177	17	23.6	12	2				250	17	23.6	16	2			

251	16	22.2	10	2	Q75SW3_ECOLI	Q75sw3 escherichia	324	16	22.2	15	1	CKX_WHEAT	P58763 triticum ae
252	16	22.2	10	2	Q7MOM6_DESDE	Q7mom6 desulfovibr	325	16	22.2	15	1	CMPI8_TOBAC	P80795 nicotiana t
253	16	22.2	11	1	POOC_PSEFL	P55173 pseudomonas	326	16	22.2	15	1	MPPI8_FAT	P81563 rattus norv
254	16	22.2	11	1	PVK1_BLACK	P83923 blaberus cr	327	16	22.2	15	2	Q9UWH4_GEURY	Q9uwh4 pyrococcus
255	16	22.2	11	1	PVK1_BLDU	P83924 blaberus du	328	16	22.2	15	2	P82207_BOWMO	P82207 bombyx mori
256	16	22.2	11	1	PVK1_BLAGI	P84561 blaberus gi	329	16	22.2	15	2	Q4YIV3_PLABE	Q4yiv3 plasmodium
257	16	22.2	11	1	PVK1_CYROPO	P84656 cyrtoceria p	330	16	22.2	15	2	Q7MJB4_VULVU	Q7mjb4 vulpes vulp
258	16	22.2	11	1	PVK1_GROPO	P83925 gromphadori	331	16	22.2	15	2	Q7MRG9_BOVIN	Q7mr9 bos taurus
259	16	22.2	11	1	PVK1_LEUMA	P83921 leucophaea	332	16	22.2	15	2	Q5XPT1_SOLTU	Q5xpt1 solanum tub
260	16	22.2	11	1	PVK1_MALCI	P83922 nauphaea c	333	16	22.2	15	2	Q05463_9PROT	Q05463 nitrosospir
261	16	22.2	11	1	PVK1_PESVR	P84657 perlephaeri	334	16	22.2	15	2	P97249_9PROT	P97249 nitrosospir
262	16	22.2	11	1	PVK1_PYCSU	P84654 pycnoscelus	335	16	22.2	15	2	Q8LI61_THERA	Q8li61 thermoanaer
263	16	22.2	11	1	PVK3_APPFU	P84661 aptera fusc	336	16	22.2	15	2	Q9RSP2_SERMA	Q9r52 seriatia ma
264	16	22.2	11	1	PVK3_BLACK	P83923 blaberus cr	337	16	22.2	15	2	Q86128_GRAHB	Q86128 vesicular s
265	16	22.2	11	1	PVK3_BLAU	P84593 blaberus du	338	16	22.2	15	2	Q9PKX5_TEV	Q9pkx5 tubacco etc
266	16	22.2	11	1	PVK3_BLAGI	P84593 blaberus gi	339	16	22.2	15	2	Q91124_MOUSE	Q91y4 mus musculu
267	16	22.2	11	1	PVK3_GROPO	P83925 gromphadori	340	15.5	21.5	15	1	UCI7_MAIZE	Q91y4 mus musculu
268	16	22.2	11	1	PVK3_LEUMA	P83921 leucophaea	341	15	20.8	8	1	CCRN_DRAVI	P80623 zea mays (m
269	16	22.2	11	1	PVK3_MALCI	P84662 nauphaea c	342	15	20.8	8	1	CCRN_DRAVI	Q9yq10 transmissib
270	16	22.2	11	1	PVK3_PANVI	P83932 panchlora v	343	15	20.8	8	1	CCRN_MACEU	P86125 dasyurus vi
271	16	22.2	11	2	Q7MBZ6_GMOU	Q31b6 candidatus	344	15	20.8	8	1	CONO_CONMU	P86126 macrophis eu
272	16	22.2	11	2	Q7MBZ6_GMOU	Q31b6 candidatus	345	15	20.8	8	1	NS3_MYCTU	P84701 conus mus (
273	16	22.2	11	2	Q9K7A4_BACHU	Q7m154 bacillus th	346	15	20.8	8	1	NS3_MYCTU	P81152 mycobacteri
274	16	22.2	12	1	XYLA_STRVN	Q9K7A4 bacillus ha	347	15	20.8	8	2	P82324_PEA	P82324 pisum sativ
275	16	22.2	12	1	YZPY_ECOLI	P14405 streptomyce	348	15	20.8	9	2	Q30822_AEGTA	Q30822 aegilops ta
276	16	22.2	12	2	Q68CUI_HUMAN	Q68cui homo sapien	349	15	20.8	9	2	Q7IEB9_HUMAN	Q7ie9 homo sapien
277	16	22.2	12	2	Q47251_ECOLI	Q47251 escherichia	350	15	20.8	9	2	Q4YIG1_PLABE	Q4yig1 plasmodium
278	16	22.2	12	2	Q84AV9_GEMTR	Q84av9 buchnera ap	351	15	20.8	9	2	Q7MYN8_BOSIN	Q7my28 bos indicus
279	16	22.2	12	2	Q69232_BHVA	Q69232 bovine hepr	352	15	20.8	9	2	Q4S652_CLOBU	Q4s62 clostridium
280	16	22.2	12	2	Q3B742_BRARE	Q3b742 brachydanio	353	15	20.8	10	1	Q6LDP7_RAT	Q6ldp7 rattus norv
281	16	22.2	12	2	Q4PU25_9CICH	Q4pu25 neolamprolo	354	15	20.8	10	2	SC41_FITCA	P84664 citrus camb
282	16	22.2	12	2	Q4PU26_9CICH	Q4pu26 neolamprolo	355	15	20.8	10	2	Q7SIH4_NEURC	Q7sih4 neurospora
283	16	22.2	12	2	Q4PU27_9CICH	Q4pu27 lepidiolamp	356	15	20.8	10	2	Q4XZ43_PLACH	Q4xz43 plasmodium
284	16	22.2	12	2	Q4PU29_9CICH	Q4pu29 variabilich	357	15	20.8	10	2	Q7RH60_PLAYO	Q7rh60 plasmodium
285	16	22.2	12	2	Q4PU30_9CICH	Q4pu30 neolamprolo	358	15	20.8	10	2	Q8WPL6_9URCO	Q8wpl6 oktopleura
286	16	22.2	12	2	Q4PU32_9CICH	Q4pu32 neolamprolo	359	15	20.8	10	2	Q38217_9CAUD	Q38217 laccococcus
287	16	22.2	12	2	Q4PU33_9CICH	Q4pu33 lepidiolamp	360	15	20.8	10	2	Q56ZK9_ARATH	Q56z9 arabidopsis
288	16	22.2	12	2	Q4PU34_9CICH	Q4pu34 altilamprol	361	15	20.8	10	2	Q7MOK7_RHOSO	Q7mok7 rhodococcus
289	16	22.2	12	2	Q4PU35_9CICH	Q4pu35 lepidiolamp	362	15	20.8	10	2	Q71YN2_MOUSE	Q71yn2 mus musculu
290	16	22.2	12	2	Q4PU41_9CICH	Q4pu41 lepidiolamp	363	15	20.8	10	2	Q9B07_ALLMT	Q9b07 alligator m
291	16	22.2	12	2	Q4PU31_9CICH	Q4pu31 lampulogus	364	15	20.8	11	1	BRKP_PHYSA	P81252 phyllomedus
292	16	22.2	12	2	Q4PU37_ALTCL	Q4pu37 altilamprol	365	15	20.8	11	1	KNL2_PHYSA	P84667 phyllomedus
293	16	22.2	12	2	Q4PU42_9CICH	Q4pu42 lepidiolamp	366	15	20.8	11	1	TKN_ELECI	P62933 eleone cir
294	16	22.2	12	2	Q4PU44_9CICH	Q4pu44 lepidiolamp	367	15	20.8	11	1	TKN_ELEMO	P62934 eleone mos
295	16	22.2	12	2	Q213J6_CHAGU	Q213j6 champsoceph	368	15	20.8	11	2	Q4X3Y5_PLACH	Q4x3y5 plasmodium
296	16	22.2	12	2	Q65027_AYMB	Q65027 avian myelo	369	15	20.8	11	2	Q4ZC6_PLABE	Q4z26 plasmodium
297	16	22.2	13	1	AH4_FROSE	P29262 prunus sero	370	15	20.8	11	2	Q9XSP2_HYLSY	Q9xsp2 hylobates s
298	16	22.2	13	1	AUR11_LITRA	P82386 littoria ran	371	15	20.8	11	2	Q9XSP5_PANTR	Q9xsp5 pan troglod
299	16	22.2	13	1	AUR12_LITRA	P82387 littoria ran	372	15	20.8	11	2	Q9XSP6_PONPY	Q9xsp6 pongo pygma
300	16	22.2	13	1	RS19_ASHYP	Q44592 ash yellow	373	15	20.8	11	2	Q9XSP7_PYGNE	Q9xsp7 pygathrix n
301	16	22.2	13	1	TEICG_RANCL	P82882 rana clamit	374	15	20.8	11	2	Q9XSP8_9PRIM	Q9xsp8 presbytis j
302	16	22.2	13	2	P87031_YEAST	P87031 saccharomyc	375	15	20.8	11	2	Q9XSP4_9PRIM	Q9xsp4 gorilla gor
303	16	22.2	13	2	Q7RSC5_PLAYO	Q7res5 plasmodium	376	15	20.8	11	2	Q6T352_QUEPE	Q6t352 quezque pet
304	16	22.2	13	2	Q32XJ6_PLEPA	Q32xj6 plecotus ra	377	15	20.8	11	2	Q70Y70_9LAMI	Q70y70 thomomys
305	16	22.2	13	2	Q7BVK6_ERWAM	Q7bv6 erwania amy	378	15	20.8	11	2	Q7TME3_MOUSE	Q7tme3 mus musculu
306	16	22.2	13	2	Q8GBU2_VIBHA	Q8gbu2 vibrio harv	379	15	20.8	11	2	Q77892_ORENI	Q77892 oreochromis
307	16	22.2	13	2	Q9AMK2_XANCP	Q9amk2 xanthomonas	380	15	20.8	11	2	Q77906_ORENI	Q77906 oreochromis
308	16	22.2	13	2	Q9RFG4_MYCNC	Q9rf4 mycoplasma	381	15	20.8	11	2	VEBP_VESNA	Q7m12 vespa manda
309	16	22.2	13	2	Q9RG00_MYCCA	Q9rg00 mycoplasma	382	15	20.8	12	1	VEBP_VESXA	Q7m12 vespa xanth
310	16	22.2	13	2	P90442_NPVSL	P90442 spodoptera	383	15	20.8	12	2	Q9UMR0_HUMAN	Q9umr0 homo sapien
311	16	22.2	14	1	HBX_OREMO	P83761 oreochromis	384	15	20.8	12	2	Q4Y2T2_PLACH	Q4y2t2 plasmodium
312	16	22.2	14	1	MCRX_METTM	P58485 methanobact	385	15	20.8	12	2	Q9BFW4_MYRTR	Q9bfw4 myriocophae
313	16	22.2	14	1	PLYBI_POLPI	P84388 polybia pau	386	15	20.8	12	2	Q70Y67_9LAMI	Q70y67 ocium giat
314	16	22.2	14	1	PLYB2_POLPI	P84389 polybia pau	387	15	20.8	12	2	Q70Y95_9LAMI	Q70y95 ocium giat
315	16	22.2	14	1	TKN1_SCHGR	P82470 schistocerc	388	15	20.8	12	2	Q8S1G4_9FLOR	Q8s1g4 halymena f
316	16	22.2	14	1	Q96KF9_HUMAN	Q96kf9 homo sapien	389	15	20.8	12	2	Q51T00_9CALI	Q51t00 notovirus s
317	16	22.2	14	2	Q7RBZ5_PLAYO	Q7rbz5 plasmodium	390	15	20.8	12	2	Q767J2_ONCKE	Q767j2 oncorhynch
318	16	22.2	14	2	P82332_PEA	P82332 pisum sativ	391	15	20.8	12	2	FLET_LIMPT	P82064 limnodonast
319	16	22.2	14	2	Q71IZ6_LACBOL	Q71iz6 lacobocill	392	15	20.8	13	1	GRA2B_POCPU	P69843 pogonoperca
320	16	22.2	14	2	Q8VU21_STRPN	Q8vu21 streptococc	393	15	20.8	13	1	GRA2B_POCPU	P69844 pogonoperca
321	16	22.2	14	2	Q9R782_BACCI	Q9r782 bacillus ii	394	15	20.8	13	1	GRAE_GRASK	P69841 grammitis
322	16	22.2	14	2	Q2MHR3_ECOLI	Q2mhr3 escherichia	395	15	20.8	13	1	TEI1BA_RANBO	P84116 rana boylii
323	16	22.2	14	2	Q73591_CHICK	Q73591 gallus gall	396	15	20.8	13	1	TEML_RANTE	P57104 rana tempor

397	15	20.8	13	2	05H8A9_HUMAN	05H8a9 homo sapien	470	14	19.4	8	1	PKK2_PERAM	P82692 periplaneta
398	15	20.8	13	2	071UN9_HUMAN	071un9 homo sapien	471	14	19.4	8	1	RS1_ERMCH	P37985 erwinia chr
399	15	20.8	13	2	07M19_GALNA	07m19 giardia lam	472	14	19.4	8	2	015895_HUMAN	P13985 homo sapien
400	15	20.8	13	2	07RPA9_PLAYO	07rpa9 plasmodium	473	14	19.4	8	2	09POK3_HUMAN	09pok3 homo sapien
401	15	20.8	13	2	09U5J3_GRYTP	09u5j3 trypanosoma	474	14	19.4	8	2	09TWE6_YANNE	09twe6 periteneis
402	15	20.8	13	2	07M373_BOVIN	07m373 bos taurus	475	14	19.4	8	2	05W4V6_YVIRU	05w4v6 bacterioph
403	15	20.8	13	2	07YRD1_BISBO	07yrd1 bison bonas	476	14	19.4	8	2	05W4V6_9CAUD	05w4v6 bacterioph
404	15	20.8	13	2	07YRI4_BOVIN	07yri4 bos taurus	477	14	19.4	8	2	05W4V8_BPR51	05w4v8 bacterioph
405	15	20.8	13	2	09TUD7_BOVIN	09tud7 bos taurus	478	14	19.4	8	2	05W4W1_9CAUD	05w4w1 bacterioph
406	15	20.8	13	2	056YV8_ARATH	056yv8 arabidopsis	479	14	19.4	8	2	05W4W2_BPR32	05w4w2 bacterioph
407	15	20.8	13	2	08WEJ3_GINBI	08wej3 ginkgo bil	480	14	19.4	8	2	05W4M4_9CAUD	05w4m4 bacterioph
408	15	20.8	13	2	0945C1_CRYCO	0945c1 cryptococi	481	14	19.4	8	2	05W4W6_YVIRU	05w4w6 bacterioph
409	15	20.8	13	2	09GCU6_YLLI1	09gcu6 veitchia ar	482	14	19.4	8	2	05W4X0_9CAUD	05w4x0 bacterioph
410	15	20.8	13	2	07M1A2_BACNO	07m1a2 bacteroides	483	14	19.4	8	2	05W4X2_YVIRU	05w4x2 bacterioph
411	15	20.8	13	2	09KHJ4_CAUCR	09khj4 caulobacter	484	14	19.4	8	2	05W4X4_YVIRU	05w4x4 bacterioph
412	15	20.8	13	2	07BEH3_MOUSE	07beh3 mus musculi	485	14	19.4	8	2	05W4X6_BPR25	05w4x6 bacterioph
413	15	20.8	13	2	02WD52_FICGH	02wd52 ficedula hy	486	14	19.4	8	2	05W4X8_BPR24	05w4x8 bacterioph
414	15	20.8	13	2	02WD53_FICPA	02wd53 ficedula pa	487	14	19.4	8	2	05W4Y0_BPR21	05w4y0 bacterioph
415	15	20.8	13	2	02WD61_FICAL	02wd61 ficedula al	488	14	19.4	8	2	05W4Y2_9CAUD	05w4y2 bacterioph
416	15	20.8	13	1	ECDC_LYMD1	P80940 lymphatria d	489	14	19.4	8	2	05W4Y4_9CAUD	05w4y4 bacterioph
417	15	20.8	14	1	MAST_VESOR	P17338 vespa orient	490	14	19.4	8	2	05W4Y6_BPR70	05w4y6 bacterioph
418	15	20.8	14	2	050845_METVO	050845 methanococc	491	14	19.4	8	2	08H9H3_9CAUD	08h9h3 bacterioph
419	15	20.8	14	2	07S2V7_NEUCR	07s2v7 neurospora	492	14	19.4	8	2	08H9H5_BPR76	08h9h5 bacterioph
420	15	20.8	14	2	09P2A2_HUMAN	09p2a2 homo sapien	493	14	19.4	8	2	08H9H6_BPR27	08h9h6 bacterioph
421	15	20.8	14	2	05WQZ8_OPICA	05wqz8 opisthoptna	494	14	19.4	8	2	08H9I2_BPR27	08h9i2 bacterioph
422	15	20.8	14	2	07RKW6_PLAYO	07rkw6 plasmodium	495	14	19.4	8	2	08H9I3_9CAUD	08h9i3 bacterioph
423	15	20.8	14	2	085CA2_STRDR	085ca2 strongyloce	496	14	19.4	8	2	08H9I4_9CAUD	08h9i4 bacterioph
424	15	20.8	14	2	085100_9ECHO	085100 strongyloce	497	14	19.4	8	2	08H9I6_BPR15	08h9i6 bacterioph
425	15	20.8	14	2	071GJ1_9HYME	071gj1 anthroipode	498	14	19.4	8	2	08H9I8_9CAUD	08h9i8 bacterioph
426	15	20.8	14	2	09SMV4_ARATH	09smv4 arabidopsis	499	14	19.4	8	2	08H9I9_BPR10	08h9i9 bacterioph
427	15	20.8	14	2	09R518_VIBAL	09r518 vibrio algi	500	14	19.4	8	2	08H9J1_BPR06	08h9j1 bacterioph
428	15	20.8	14	2	0661E1_BORGA	0661e1 borrelia ga	501	14	19.4	8	2	08H9J1_BPR03	08h9j1 bacterioph
429	15	20.8	14	2	09ZOG5_MOUSE	09zogs mus musculi	502	14	19.4	8	2	08H9J5_9CAUD	08h9j5 bacterioph
430	15	20.8	14	2	06JTV7_ONCMY	06jtv7 oncorhynch	503	14	19.4	8	2	08H9J7_BPR02	08h9j7 bacterioph
431	15	20.8	14	2	02OF76_MEIGA	02of76 melagris g	504	14	19.4	8	2	08H9J9_BPR15	08h9j9 bacterioph
432	15	20.8	14	2	010Z34_9HIV1	010z34 human immun	505	14	19.4	8	2	08H9J9_BPR15	08h9j9 bacterioph
433	15	20.8	15	1	APFL_MALPA	P83141 malva parvi	506	14	19.4	8	2	08H9K4_BPR3	08h9k4 bacterioph
434	15	20.8	15	1	MCPI6_LYCES	P80812 lycopersico	507	14	19.4	8	2	05DOK1_9LILI	05dok1 toxococcus
435	15	20.8	15	1	04W378_9LECA	04w378 mechansarc	508	14	19.4	8	2	05DOK8_9LILI	05dok8 hydatistele
436	15	20.8	15	2	07M4Y5_FUSSP	07m4y5 fusarium sp	509	14	19.4	8	2	05DOK7_9LILI	05dok7 gullibia cos
437	15	20.8	15	2	013377_HUMAN	013377 homo sapien	510	14	19.4	8	2	05DON2_9LILI	05don2 gnomophyllu
438	15	20.8	15	2	04X8U7_PLACH	04x8u7 plasmodium	511	14	19.4	8	2	05DOK5_9LILI	05dok5 areca triana
439	15	20.8	15	2	04YFG1_PLABE	04yfg1 plasmodium	512	14	19.4	8	2	05DOK9_9LILI	05dok9 cythosperma
440	15	20.8	15	2	05K6Q7_CRAGI	05k6q7 crassostrea	513	14	19.4	8	2	045889_CLOBO	045889 clostridium
441	15	20.8	15	2	06JCR8_9HEMI	06jcr8 bemisia arg	515	14	19.4	8	2	08G940_BORBU	08g940 borrelia bu
442	15	20.8	15	2	07M3B5_VULVU	07m3b5 vulpes vulp	516	14	19.4	8	2	09R4M3_ENTPA	09r4m3 enterococcu
443	15	20.8	15	2	09TRR8_RABIT	09trr8 oryctolagus	517	14	19.4	8	2	08GL21_BORBU	08gl21 thubob
444	15	20.8	15	2	042223_ARATH	042223 arabidopsis	518	14	19.4	9	1	C6A1_THUOB	06A1 thubob
445	15	20.8	15	2	04PZV5_JUSAM	04pzv5 justicia am	519	14	19.4	9	1	FARS_BENNO	07FAR5 benno
446	15	20.8	15	2	07OY59_ROSOF	07oy59 rosmarinus	520	14	19.4	9	1	FLA2_TREHY	07FLA2 trehy
447	15	20.8	15	2	08S136_9MAGN	08s136 chlamydom	521	14	19.4	9	2	07RYB8_NEUCR	07ryb8 neurospora
448	15	20.8	15	2	09T202_CHLRE	09t202 chlamydom	522	14	19.4	9	2	07S1B2_NEUCR	07s1b2 neurospora
449	15	20.8	15	2	09R544_MYCBO	09r544 mycobacteri	523	14	19.4	9	2	03YNA4_DROME	03yna4 dirosophila
450	15	20.8	15	2	019468_MOUSE	019468 mus musculi	524	14	19.4	9	2	07RAE2_PLAYO	07rae2 plasmodium
451	15	20.8	15	2	08B175_MOUSE	08b175 mus musculi	525	14	19.4	9	2	05ZES4_BOVIN	05zes4 bos taurus
452	15	20.8	15	2	03MUG6_MESAU	03mug6 mesocricetu	526	14	19.4	9	2	08HYZ2_CANPA	08hyz2 canis famli
453	15	20.8	15	2	09OV01_9MURI	09ov01 mus sp. 16	527	14	19.4	9	2	09TUYO_MONDO	09tuyo monodelphis
454	15	20.8	15	2	09OV17_9MURI	09ov17 rattus sp.	528	14	19.4	9	2	05DQJ7_9LILI	05dqj7 nenga puntil
455	15	20.8	15	2	09OVNO_9MURI	09ovno rattus sp.	529	14	19.4	9	2	05DQK7_9LILI	05dqk7 hydatistele
456	15	20.8	15	2	P83333_ONCMY	P83333 oncorhynch	530	14	19.4	9	2	05DQW6_9LILI	05dqw6 gnomophyllu
457	15	20.8	15	2	07LZ20_CHICK	07l220 gallus galli	531	14	19.4	9	2	05DON8_9LILI	05don8 gnomophyllu
458	15	20.8	15	2	09TH04_GRUAM	09th04 gallus americ	532	14	19.4	9	2	05DON9_9LILI	05don9 gnomophyllu
459	15	20.8	15	2	09TRU9_BOVIN	09tru9 bos taurus	533	14	19.4	9	2	05DON4_9LILI	05don4 areca rheop
460	14.5	20.1	12	2	PPH2_LYCES	P83379 lycopersico	534	14	19.4	9	2	05DON6_9LILI	05don6 areca carec
461	14	19.4	7	1	UNO6_PINES	P81675 pinus pinas	535	14	19.4	9	2	05DQPI_9LILI	05dqpi manictaria s
462	14	19.4	7	1	015905_HUMAN	015905 homo sapien	536	14	19.4	9	2	07OYB3_9LAMI	07oyb3 leopoldantia
463	14	19.4	7	2	08GL04_BORBU	08gl04 borrelia bu	537	14	19.4	9	2	05DOP2_9LILI	05dop2 kentriopsis
464	14	19.4	8	1	ALLI5_CARMA	P81819 carcinus ma	538	14	19.4	9	2	05DOP3_9LILI	05dop3 ignanura wa
465	14	19.4	8	1	ALLI6_CARMA	P81819 carcinus ma	539	14	19.4	9	2	05DOP4_9LILI	05dop4 amandara de
466	14	19.4	8	1	ALL4_CYDPO	P41840 calliphora	540	14	19.4	9	2	05DOP6_9LILI	05dop6 borrelia bu
467	14	19.4	8	1	ALL4_CYDPO	P41840 calliphora	541	14	19.4	9	2	08GL26_BORBU	08gl26 borrelia bu
468	14	19.4	8	1	ALL4_CYDPO	P41840 calliphora	542	14	19.4	9	2	08GL31_BORBU	08gl31 borrelia bu
469	14	19.4	8	1	ALL4_CYDPO	P41840 calliphora	543	14	19.4	9	2	08GL31_BORBU	08gl31 borrelia bu

543	14	19.4	9	2	Q9R3C4	BORBU	Q9r9c4	borrella bu	616	14	19.4	12	2	Q673J1	PANPA	Q673j1	pan paniscu
544	14	19.4	9	2	Q3TMU8	MOUSE	Q3tm8	mus musculus	617	14	19.4	12	2	Q673J2	PANTR	Q673j2	pan troglod
545	14	19.4	9	2	Q4MBQ9	MOUSE	Q4mb9	mus musculus	618	14	19.4	12	2	Q9T2U3	BOVIN	Q9t2u3	bos taurus
546	14	19.4	9	2	Q6YR34	RAT	Q6y34	rattus norv	619	14	19.4	12	2	Q9TRV4	GCETA	Q9trv4	sus sp. ins
547	14	19.4	9	2	Q9QZAT	MOUSE	Q9qzat	mus musculus	620	14	19.4	12	2	P940I1	ARATH	P940i1	arabidopsis
548	14	19.4	9	2	Q8JFA6	FICHY	Q8jfa6	ficedula hy	621	14	19.4	12	2	Q2T1B0	SOYBN	Q2t1b0	glycine max
549	14	19.4	9	2	Q8JFA7	FICHL	Q8jfa7	ficedula al	622	14	19.4	12	2	Q41B56	MAIZE	Q41b56	zea mays (m
550	14	19.4	10	1	COX81	SHEEP	P80337	ovis aries	623	14	19.4	12	2	Q5DQK4	GLILI	Q5dql5	hydrastelle
551	14	19.4	10	1	MBSP	SAUMA	P84476	saurea wan	624	14	19.4	12	2	Q5DQK5	GLILI	Q5dql5	hydrastelle
552	14	19.4	10	1	SC64	TITCA	P84562	titusd camb	625	14	19.4	12	2	Q5DQK5	GLILI	Q5dql5	hydrastelle
553	14	19.4	10	1	TEBK	RANTE	P56923	rana tempor	626	14	19.4	12	2	Q5DQK1	GLILI	Q5dql5	hydrastelle
554	14	19.4	10	1	UHA3	HUMAN	P40930	homo sapien	627	14	19.4	12	2	Q5KSP0	SYMFO	Q5ksp0	symlocarpu
555	14	19.4	10	2	Q7S225	NEUCR	Q7s225	neurospora	628	14	19.4	12	2	Q7MIU3	ORYSA	Q7miu3	oryza sativ
556	14	19.4	10	2	Q7S2K0	NEUCR	Q7s2k0	neurospora	629	14	19.4	12	2	Q7M2G3	VICPA	Q7m2g3	vicia faba
557	14	19.4	10	2	Q7LDT7	HUMAN	Q7ldt7	homo sapien	630	14	19.4	12	2	Q9R5A9	GCARY	Q9r5a9	silene aega
558	14	19.4	10	2	Q4X4H2	PLACH	Q4x4h2	plasmodium	631	14	19.4	12	2	Q5DQK7	GLILI	Q5dql7	socratea ex
559	14	19.4	10	2	Q4X6X5	PLACH	Q4x6x5	plasmodium	632	14	19.4	12	2	Q500I9	MYCLE	Q500i9	mycobacteri
560	14	19.4	10	2	Q7M4C9	HEMPU	Q7m4c9	hemiceleot	633	14	19.4	12	2	Q83U71	SALET	Q83u71	salmonella
561	14	19.4	10	2	Q7M4D8	ANTCR	Q7m4d8	anthocidari	634	14	19.4	12	2	Q9S4K7	ECOLI	Q9s4k7	escherichia
562	14	19.4	10	2	Q7M2U1	BOVIN	Q7m2u1	bos taurus	635	14	19.4	12	2	Q9X636	KLB0X	Q9x636	klebsiella
563	14	19.4	10	2	Q67B26	9CAUD	Q67b26	bacterioph	636	14	19.4	12	2	Q3TRQ3	MOUSE	Q3trq3	mus musculus
564	14	19.4	10	2	Q5DQJ5	GLILI	Q5dqj5	siphokentia	637	14	19.4	12	2	Q2Q8P5	PHYFS	Q2q8p5	phyllioscopu
565	14	19.4	10	2	Q5DQJ6	GLILI	Q5dqj6	pinanga cor	638	14	19.4	12	2	Q2Q8P6	PHYBO	Q2q8p6	phyllioscopu
566	14	19.4	10	2	Q5DQK0	GLILI	Q5dqk0	loxococcus	639	14	19.4	12	2	Q2Q8P7	PHYTO	Q2q8p7	phyllioscopu
567	14	19.4	10	2	Q5DQK0	GLILI	Q5dqk0	gububia lon	640	14	19.4	12	2	Q2Q8P8	PHYTO	Q2q8p8	phyllioscopu
568	14	19.4	10	2	Q5DQK5	GLILI	Q5dqk5	gromophyllu	641	14	19.4	12	2	Q2Q8P9	PHYTO	Q2q8p9	phyllioscopu
569	14	19.4	10	2	Q5DQK5	GLILI	Q5dqk5	gromophyllu	642	14	19.4	12	2	Q2Q8Q0	PHYCO	Q2q8q0	phyllioscopu
570	14	19.4	10	2	Q5DQK8	GLILI	Q5dqk8	reiharticia	643	14	19.4	12	2	Q2Q8Q2	PHYCO	Q2q8q2	phyllioscopu
571	14	19.4	10	2	Q5DQK0	GLILI	Q5dqk0	normalhya n	644	14	19.4	12	2	Q2Q8Q3	PHYBE	Q2q8q3	phyllioscopu
572	14	19.4	10	2	Q85V66	EUCAR	Q85v66	eucalyptus	645	14	19.4	12	2	Q2Q8R6	PHYTC	Q2q8r6	phyllioscopu
573	14	19.4	10	2	Q9FS93	GCARY	Q9fs93	silene pent	646	14	19.4	12	2	Q5ERY2	GLILI	Q5ery2	human immun
574	14	19.4	10	2	Q5DQK5	GLILI	Q5dqk5	areca conc	647	14	19.4	12	2	Q5ERY2	GLILI	Q5ery2	human immun
575	14	19.4	10	2	Q5DQK2	GLILI	Q5dqk2	hydrastelle	648	14	19.4	12	2	Q5ERT4	GLILI	Q5ert4	human immun
576	14	19.4	10	2	Q52837	RHILE	Q52837	rhizobium l	649	14	19.4	12	2	Q5ERT6	GLILI	Q5ert6	human immun
577	14	19.4	10	2	Q5D4Q3	9RHOO	Q5d4q3	azospira or	650	14	19.4	12	2	Q5ERT8	GLILI	Q5ert8	human immun
578	14	19.4	10	2	Q5D4Q4	9RHOO	Q5d4q4	dechloromon	651	14	19.4	12	2	Q5EUV0	GLILI	Q5euvo	human immun
579	14	19.4	10	2	Q9JN49	STRAU	Q9j49	staphylococ	652	14	19.4	12	2	Q5EUV2	GLILI	Q5euvo2	human immun
580	14	19.4	10	2	Q9LSM6	LIBAC	Q9ls6	liberibacte	653	14	19.4	12	2	Q5EUV10	GLILI	Q5eu10	human immun
581	14	19.4	10	2	Q8G8W5	BORBU	Q8g8w5	borrella bu	654	14	19.4	12	2	Q5EUV12	GLILI	Q5eu12	human immun
582	14	19.4	10	2	Q9JLI5	MOUSE	Q9jli5	mus musculus	655	14	19.4	12	2	Q5EUV20	GLILI	Q5eu20	human immun
583	14	19.4	10	2	Q2WDB9	FICHL	Q2wdb9	ficedula al	656	14	19.4	12	2	Q5EUV22	GLILI	Q5eu22	human immun
584	14	19.4	10	2	Q9PRY8	TRISC	Q9py8	trilakis scy	657	14	19.4	12	2	Q5EUV24	GLILI	Q5eu24	human immun
585	14	19.4	11	1	BRK	MEGFL	P12797	megascollia	658	14	19.4	12	2	Q90QD1	9HIV1	Q90qd1	human immun
586	14	19.4	11	1	RS30	ONCMY	P83328	oncorhynch	659	14	19.4	12	2	Q9JCES	GLILI	Q9jces	human immun
587	14	19.4	11	2	Q9UR55	PICAN	Q9ur55	pichia angu	660	14	19.4	13	1	TEICA	RANCL	TEICA	oryza sativ
588	14	19.4	11	2	Q9UR55	PICAN	Q9ur55	pichia angu	661	14	19.4	13	1	TEICD	RANCL	TEICD	oryza sativ
589	14	19.4	11	2	Q4X8K4	PLACH	Q4x8k4	plasmodium	662	14	19.4	13	1	TEICE	RANCL	TEICE	clamit
590	14	19.4	11	2	Q4YD43	PLABE	Q4yd43	plasmodium	663	14	19.4	13	1	TEILA	RANLU	TEILA	rana luteiv
591	14	19.4	11	2	Q6LC30	FASHE	Q6lc30	fasciola he	664	14	19.4	13	2	Q508J3	METVO	Q508j3	methanococc
592	14	19.4	11	2	Q7RH63	PLAYO	Q7rh63	plasmodium	665	14	19.4	13	2	Q7M4Y6	FUSSP	Q7m4y6	fuesarium ap
593	14	19.4	11	2	Q45X12	9ELTH	Q45x12	elephantulu	666	14	19.4	13	2	Q8WYB7	HUMAN	Q8wyb7	homo sapien
594	14	19.4	11	2	Q6JDK6	CANFA	Q6jdk6	canis famli	667	14	19.4	13	2	Q9UM84	HUMAN	Q9um84	homo sapien
595	14	19.4	11	2	Q7M374	BOVIN	Q7m374	bos taurus	668	14	19.4	13	2	Q4QV26	9BIVA	Q4qv26	cridacna gi
596	14	19.4	11	2	Q9TQSO	BOVIN	Q9tqso	bos taurus	669	14	19.4	13	2	Q50L81	9DIPR	Q50l81	drosophila
597	14	19.4	11	2	Q5DQJ6	GLILI	Q5dqj6	hydrastelle	670	14	19.4	13	2	Q6SE60	DROSI	Q6se60	drosophila
598	14	19.4	11	2	Q5DQJ6	GLILI	Q5dqj6	gububia pal	671	14	19.4	13	2	Q812E2	PLAF7	Q812e2	plasmodium
599	14	19.4	11	2	Q7X9Y3	CUCSA	Q7x9y3	cucumis sat	672	14	19.4	13	2	Q94RE2	LEPSE	Q94re2	leptomans
600	14	19.4	11	2	Q8RV30	MAIZE	Q8rv30	zea mays (m	673	14	19.4	13	2	Q2TIL5	GLILI	Q2til5	gububia cy1
601	14	19.4	11	2	Q44237	9NOST	Q44237	anabaena sp	674	14	19.4	13	2	Q5DQJ9	GLILI	Q5dqj9	hydrastelle
602	14	19.4	11	2	Q8GJ19	BORBU	Q8gj19	borrella bu	675	14	19.4	13	2	Q5DQJ9	GLILI	Q5dqj9	gububia mac
603	14	19.4	11	2	Q8GJ24	BORBU	Q8gj24	borrella bu	676	14	19.4	13	2	Q5DQJ9	GLILI	Q5dqj9	gububia mac
604	14	19.4	11	2	Q61797	MOUSE	Q61797	mus musculus	677	14	19.4	13	2	Q5DQK4	GLILI	Q5dqk4	gromophyllu
605	14	19.4	11	2	Q6R206	ONCMY	Q6r206	oncorhynch	678	14	19.4	13	2	Q7DMV2	ACTUDE	Q7dmv2	actinidia d
606	14	19.4	11	2	Q85620	MUYMO	Q85620	moloney mut	679	14	19.4	13	2	Q9FS94	9GCARY	Q9fs94	silene pent
607	14	19.4	12	1	P4R7	PENMO	P83322	penaeus mon	680	14	19.4	13	2	Q9FSAB	SILBA	Q9fsab	silene bacc
608	14	19.4	12	2	Q16405	HUMAN	Q16405	homo sapien	681	14	19.4	13	2	Q798K6	STRPN	Q798k6	streplococc
609	14	19.4	12	2	Q4XWZ8	PLACH	Q4xwz8	plasmodium	682	14	19.4	13	2	Q9R8R9	STRPY	Q9r8r9	streplococc
610	14	19.4	12	2	Q8TQV6	APIME	Q8tqv6	apis mellif	683	14	19.4	13	2	Q9XBY0	9BACT	Q9xbv0	nitrogen-fi
611	14	19.4	12	2	Q9TWT4	LYNST	Q9tw4	lymaea stra	684	14	19.4	13	2	Q47607	ECOLI	Q47607	escherichia
612	14	19.4	12	2	Q673I4	PAPCY	Q673i4	papio cynoc	685	14	19.4	13	2	Q9R3R3	BORBU	Q9r3r3	borrella bu
613	14	19.4	12	2	Q673I5	PAPPA	Q673i5	papio papio	686	14	19.4	13	2	Q8B5N4	9BACU	Q8b5n4	epinotia ap
614	14	19.4	12	2	Q673I7	PONPY	Q673i7	pongo pygma	687	14	19.4	13	2	Q2Q8P4	PHYFS	Q2q8p4	phyllioscopu
615	14	19.4	12	2	Q673I9	9PRIM	Q673i9	gorilla gor	688	14	19.4	13	2	Q2WDT0	FICHY	Q2wdt0	ficedula hy

689	14	19.4	13	2	Q2WDT1_FICPA	Q2wdt1 ficedula pa
690	14	19.4	13	2	Q2WDT8_FICAL	Q2wdt8 ficedula al
691	14	19.4	13	2	Q6746_GRETR	Q6746 equine infe
692	14	19.4	13	2	Q86327_GRETR	Q86327 rous sarcom
693	14	19.4	13	2	Q86328_GRETR	Q86328 rous sarcom
694	14	19.4	14	1	COCO_LIMPO	P35586 limulub pol
695	14	19.4	14	1	CWFO9_LYCES	P80806 lycopersico
696	14	19.4	14	1	GLPK_STRGR	P25013 streptomyce
697	14	19.4	14	1	HLP1_HYLPV	P84922 hyia basca
698	14	19.4	14	1	MAST_VESBA	P21654 vespa puaa
699	14	19.4	14	1	MAST_VESLE	P01514 vespula lew
700	14	19.4	14	1	MAST_VESMA	P04205 vespa manda
701	14	19.4	14	1	MAST_VESXA	P01515 vespa xanth
702	14	19.4	14	1	MCRZ_METTM	P58816 methanobact
703	14	19.4	14	1	RS19_PPMBP	P52093 pigeon pea
704	14	19.4	14	1	TEILE_RANLU	P82831 rana luteiv
705	14	19.4	14	1	Q2KGV1_MAGGR	Q2kqv1 magnaporthe
706	14	19.4	14	2	Q93057_HUMAN	Q93057 homo sapien
707	14	19.4	14	2	Q9P0K5_HUMAN	Q9p0k5 homo sapien
708	14	19.4	14	2	P82209_BOMMO	P82209 bombyx mori
709	14	19.4	14	2	Q50L76_DROAN	Q50L76 drosophila
710	14	19.4	14	2	Q7REF3_PLAYO	Q7ref3 plasmodium
711	14	19.4	14	2	Q6G3C0_GDIPT	Q6g3c0 calliphora
712	14	19.4	14	2	Q7JGT8_9HYME	Q7jgt8 andrena bto
713	14	19.4	14	2	Q7M385_PIG	Q7m385 sus scrofa
714	14	19.4	14	2	Q8HYM2_FELCA	Q8hym2 felis silve
715	14	19.4	14	2	Q9TR83_PIG	Q9tr83 sus scrofa
716	14	19.4	14	2	Q67B14_9CAUD	Q67b14 bacterioph
717	14	19.4	14	2	P84491_CUCMA	P84491 cucurbita m
718	14	19.4	14	2	Q5DOK_9LILI	Q5dok9 hydrataete
719	14	19.4	14	2	Q5DOL_9LILI	Q5dol10 hydrataete
720	14	19.4	14	2	Q5DOL_9LILI	Q5dol10 hydrataete
721	14	19.4	14	2	Q5DOL_9LILI	Q5dol10 hydrataete
722	14	19.4	14	2	Q5DOL_9LILI	Q5dol10 hydrataete
723	14	19.4	14	2	Q5DOL_9LILI	Q5dol10 hydrataete
724	14	19.4	14	2	Q7M1G6_AVESA	Q7m1g6 avena sativ
725	14	19.4	14	2	Q9RS91_9CARY	Q9rs91 silene sedo
726	14	19.4	14	2	Q9RS95_9CARY	Q9rs95 silene pent
727	14	19.4	14	2	Q9RSB1_9CARY	Q9rsb1 silene aega
728	14	19.4	14	2	Q9LEH4_HORVU	Q9leh4 hordeum vul
729	14	19.4	14	2	Q45872_CLOBO	Q45872 clostridium
730	14	19.4	14	2	Q9R225_CAMJE	Q9r225 campylobact
731	14	19.4	14	2	Q9RW79_CAMCO	Q9rw79 campylobact
732	14	19.4	14	2	Q9ZB42_STRPY	Q9zb42 streptococc
733	14	19.4	14	2	Q9PMT9_CAMJE	Q9pmt9 campylobact
734	14	19.4	14	2	P70319_MOUSE	P70319 mus musculu
735	14	19.4	14	2	Q7M0S8_MOUSE	Q7m0s8 mus musculu
736	14	19.4	14	2	P70007_XENLA	P70007 xenopus lae
737	14	19.4	14	2	Q20801_PHYCO	Q20801 phylococpu
738	14	19.4	14	2	Q208R4_PHYTC	Q208r4 phylococpu
739	14	19.4	15	1	ACPE_WHEAT	P83184 tritictum ae
740	14	19.4	15	1	CWP28_LYCES	P80824 lycopersico
741	14	19.4	15	1	FGF1_CANFA	P18651 canis famli
742	14	19.4	15	1	MPAO2_ORYSA	P83466 oryza sativ
743	14	19.4	15	1	RL11_STRAU	O94520 streptomyce
744	14	19.4	15	2	Q9UW63_THELI	Q9uw63 thermococcu
745	14	19.4	15	2	Q9UWH3_THELI	Q9uwh3 thermococcu
746	14	19.4	15	2	Q7M4X6_FUSSP	Q7m4x6 fusarium sp
747	14	19.4	15	2	Q7S459_NEUCR	Q7s459 fusarium sp
748	14	19.4	15	2	Q7SH11_NEUCR	Q7sh11 neurospora
749	14	19.4	15	2	Q9UR64_PLEOS	Q9ur64 pleurotus o
750	14	19.4	15	2	Q9UR72_TRIHA	Q9ur72 trichoderma
751	14	19.4	15	2	Q16158_HUMAN	Q16158 homo sapien
752	14	19.4	15	2	Q6LC13_HUMAN	Q6lc13 homo sapien
753	14	19.4	15	2	Q6TARI_HUMAN	Q6tari homo sapien
754	14	19.4	15	2	Q7M4R1_HUMAN	Q7m4r1 homo sapien
755	14	19.4	15	2	Q7M4S6_HUMAN	Q7m4s6 homo sapien
756	14	19.4	15	2	Q86VY8_HUMAN	Q86vy8 homo sapien
757	14	19.4	15	2	Q8TC57_HUMAN	Q8tc57 homo sapien
758	14	19.4	15	2	Q9TNP2_HUMAN	Q9tnp2 homo sapien
759	14	19.4	15	2	Q9UCB9_HUMAN	Q9ucb9 homo sapien
760	14	19.4	15	2	Q9UCV8_HUMAN	Q9ucv8 homo sapien
761	14	19.4	15	2	Q4XQUS_PLACH	Q4xqus plasmodium

762	14	19.4	15	2	Q4YF12_PLABE	Q4yf12 plasmodium
763	14	19.4	15	2	Q4YUB4_PLABE	Q4yub4 plasmodium
764	14	19.4	15	2	Q6SLH8_CAEEL	Q6slh8 caenorhabd
765	14	19.4	15	2	Q7R6M8_PLAYO	Q7r6m8 plasmodium
766	14	19.4	15	2	Q9TWFS_9CARY	Q9twfs attemia (br
767	14	19.4	15	2	Q7IGM2_9HYME	Q7igm2 andrena n.
768	14	19.4	15	2	Q7IGV6_9HYME	Q7igv6 andrena sim
769	14	19.4	15	2	Q4G3Y8_MACMU	Q4g3y8 andrena aur
770	14	19.4	15	2	Q9YQOS_BOVIN	Q9yqos macaca mula
771	14	19.4	15	2	Q5DQMI_9LILI	Q5dqmi bos taurus
772	14	19.4	15	2	Q6Z263_9CARY	Q6z263 silene ion
773	14	19.4	15	2	Q6Z274_9CARY	Q6z274 silene nigr
774	14	19.4	15	2	Q6Z276_LYCHC	Q6z276 lychnie flo
775	14	19.4	15	2	Q6Z277_9CARY	Q6z277 silene cha
776	14	19.4	15	2	Q7DLPI_SOLUT	Q7dipi solanum tub
777	14	19.4	15	2	Q7M1S8_ORYSA	Q7m1s8 oryza sativ
778	14	19.4	15	2	Q9FEI3_9CARY	Q9fei3 silene aega
779	14	19.4	15	2	Q9FEI4_9CARY	Q9fei4 silene pent
780	14	19.4	15	2	Q9FEI5_9CARY	Q9fei5 silene sedo
781	14	19.4	15	2	Q9FS80_9CARY	Q9fs80 silene zava
782	14	19.4	15	2	Q9FS98_9CARY	Q9fs98 silene iaco
783	14	19.4	15	2	Q9FS99_9CARY	Q9fs99 silene inte
784	14	19.4	15	2	Q9FSB5_9CARY	Q9fsb5 silene haus
785	14	19.4	15	2	Q9FSB6_9CARY	Q9fsb6 silene cryp
786	14	19.4	15	2	Q9FSB7_9CARY	Q9fsb7 silene aega
787	14	19.4	15	2	Q9SAP4_SOLUT	Q9sap4 solanum tub
788	14	19.4	15	2	Q9SAP4_SOLUT	Q9sap4 solanum tub
789	14	19.4	15	2	Q9SAP4_SOLUT	Q9sap4 solanum tub
790	14	19.4	15	2	Q9SAP4_SOLUT	Q9sap4 solanum tub
791	14	19.4	15	2	Q3IXN5_SHIBS	Q3ixn5 shigella bo
792	14	19.4	15	2	Q3IYP6_SHISS	Q3iyp6 shigella so
793	14	19.4	15	2	Q46013_CAVCR	Q46013 callobacter
794	14	19.4	15	2	Q8X2E0_ECOS7	Q8x2e0 escherichia
795	14	19.4	15	2	Q9R4D6_ECOLI	Q9r4d6 escherichia
796	14	19.4	15	2	Q9R4M8_BACTI	Q9r4m8 bacillus fi
797	14	19.4	15	2	Q9R533_PSEBA	Q9r533 pseudomonas
798	14	19.4	15	2	Q9R545_MYCBO	Q9r545 mycobacteri
799	14	19.4	15	2	Q9R548_MYCBO	Q9r548 mycobacteri
800	14	19.4	15	2	Q2MH50_ECOLI	Q2mh50 escherichia

ALIGNMENTS

RESULT 1
 Q7M4W9_FLAVE PRELIMINARY; PRT; 14 AA.
 AC Q7M4W9, 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Protein PF3 (Fragment).
 OS Flammulina velutipes.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 CC Agaricales; Tricholomataceae; Flammulina.
 OX NCBI_TaxID=38945;
 RP PROTEIN SEQUENCE.
 RA Sakamoto Y., Ando A., Tamai Y., Miura K.;
 RL Submitted (NOV-1999) to the PIR data bank.
 CC
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 CC
 DR PIR; C59137; C59137.
 FT NON_TER 1
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1542 MW; 543980871D704053 CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No 3.8e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVA 6
 Db 9 VPFSIS 14

RESULT 2

Q798U8_STROR PRELIMINARY; PRT; 15 AA.
 AC Q798U8_07-FEB-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DE Adenosine triphosphatase (EC 3.6.1.3) (Fragment).
 GN Name:atpA;
 OS Streptococcus oralis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus.
 OX NCBI_TaxID=1303;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCTC 11427;
 RA Renoll A., Munoz R., Garcia E., de la Campa A.G.;
 RT Molecular basis of the optochin-sensitive phenotype of pneumococcus:
 RT characterization of the genes encoding the F0 complex of the
 RT Streptococcus pneumoniae and Streptococcus oralis H(+)-ATPases.";
 RL Mol. Microbiol. 12:587-598(1994).
 CC -----
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 CC -----
 DR EMBL; Z26853; CAAB1457.1; -: Genomic DNA.
 DR GO; GO:0042624; F:ATPase activity, uncoupled; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 DM Hydrolyase.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1670 MW; 0ADE2A58DBD9D248 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 6.3e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15
 Db 1 LSSMYLG 7

RESULT 3

MDAR2 SOYBN
 ID MDAR2 SOYBN STANDARD; PRT; 10 AA.
 AC Q95926;
 DT 19-JUL-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Monodehydroascorbate reductase II (EC 1.6.5.4) (MDARII) (MR11)
 DE (Ascorbate free radical reductase II) (AFR reductase II) (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP PROTEIN SEQUENCE, CATALYTIC ACTIVITY, AND COFACTOR.
 RC STRAIN=cv. Williams; TISSUE=root nodules;
 RX MEDLINE=92088257; PubMed=1727643;
 RA Dalton D.A.; Langeberg L.; Robbins M.;
 RT "Purification and characterization of monodehydroascorbate reductase
 RT from soybean root nodules.";
 RL Arch. Biochem. Biophys. 292:281-286(1992).
 CC -1- FUNCTION: Catalyzes the conversion of monodehydroascorbate to
 CC ascorbate, oxidizing NADH in the process.
 CC -1- CATALYTIC ACTIVITY: NADH + 2 monodehydroascorbate = NAD(+) + 2

CC ascorbate.
 CC -1- COFACTOR: FAD.
 CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
 CC Kinetic parameters:
 CC KM=5.6 uM for NADH;
 CC KM=150 uM for NADPH;
 CC KM=7 uM for monodehydroascorbate;
 CC Vmax=288 umol/min/mg enzyme for NADH oxidation reaction;
 CC pH dependence:
 CC Optimum pH is 8.0-9.0;
 CC -1- SIMILARITY: Belongs to the FAD-dependent oxidoreductase family.

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 CC -----
 DR PIR; A44871; A44871.
 KW Direct protein sequencing; FAD; Flavoprotein; NAD; Oxidoreductase;
 KW Redox-active center.
 FT CHAIN <1
 FT NP_BIND 5 >10 Monodehydroascorbate reductase II.
 FT NON_TER 1 1 /FTID=PRO_0000209144.
 FT NON_TER 10 10 FAD (ADP part) (By similarity).
 SQ SEQUENCE 10 AA; 1153 MW; 848025504B5339D1 CRC64;

Query Match 31.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.3e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLYLG 15
 Db 1 AKTFKYLILG 10

RESULT 4

CRBL_VESOR
 ID CRBL_VESOR STANDARD; PRT; 14 AA.
 AC P17236;
 DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
 DT 01-AUG-1990, sequence version 1.
 DT 07-FEB-2006, entry version 31.
 DE Histamine-releasing peptide 2 (Histamine-releasing peptide II) (HR-II).
 DE Vespa orientalis (Oriental hornet).
 OS Vespa orientalis (Oriental hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7447;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom.
 RA Miroschnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
 RA Rozyanov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the
 RT venom of Vespa orientalis hornet.";
 RL Bioorg. Khim. 7:1467-1477(1981).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 CC of neutrophils.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the MCD family. Crabrolin subfamily.

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 CC -----
 DR PIR; JN0390; JN0390.
 KW Amidation; Chemotaxis; Direct protein sequencing;
 KW Mast cell degranulation; Sensory transduction.
 FT PEPTIDE 1 14 /FTID=PRO_0000044048.
 FT MOD_RES 14 14 Leucine amide.
 SQ SEQUENCE 14 AA; 1524 MW; 22015B4A6CEDFD38 CRC64;

RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda A.H., van Nijmegen E., Verardo R., Wei C.L., Yeai K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Mahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawaji J.,
 RA Hayashizaki Y.;
 RA "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX PubMed=16141073; DOI=10.1126/science.11112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RT (Genome Network Core Team) and the FANTOM Consortium;
 RL "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Bettsel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazar K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gusticich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirose-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasuniishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Watanabe Y.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bashir J.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
 RA Gusticich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehima J., Mazzarelli U., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20350913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume M., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Imotani K., Itoh M., Kanagawa S.,
 RA Nishiyori H., Nomura K., Ohno M., Murata M., Nakamura M., Niimomiya N.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; AK160958; BAB36114.1; -; mRNA.
 CC
 CC MG1; MG1700014; Sorb1.
 DR GO: GO:0001725; C:stress fiber; IDA.
 DR GO: GO:0005175; F:protein binding; IDA.
 DR GO: GO:000515; F:protein binding; IPT.
 DR GO: GO:0019901; F:protein kinase binding; IDA.
 FT NON TER 1
 FT 1
 SQ SEQUENCE 14 AA; 1616 MW; 06E511A930EF0554 CRC64;
 Query Match 31.9%; Score 23; DB 2; Length 14;
 Best Local Similarity 83.3%; Pred. No. 9e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 9 VKSLY 14
 Db 9 VKPLV 14
 RESULT 8
 P82858_9BAST PRELIMINARY; PRT; 8 AA.
 AC P82858;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DE 07-FEB-2006, entry version 11.
 OS Urethra (EC 1.7.3.3) (Urate oxidase) (Fragment).
 OC Puccinia recondita f. sp. triseti.
 OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
 OC Uredinales; Pucciniaaceae; Puccinia.
 OX NCBI_TaxID=142679;
 [1]

RP PROTEIN SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
RC TISSUE=SPORE;
RA Aguilar M., Montalbini P., Pineda M.;
RL Submitted (NOV-2000) to Swiss-Prot.
CC -!- FUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
AND FUNGI.
CC -!- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
CC -!- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: GERMINATION.
CC -!- SIMILARITY: BELONGS TO THE URICASE FAMILY.

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DR GO: GO:0005777; C:peroxisome; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0004846; F:urate oxidase activity; IEA.
DR GO: GO:0006144; P:purine base metabolism; IEA.
DR InterPro: IPR002042; Uricase.
DR PROSITE: PS00366; URICASE; PARTIAL.
KW Oxidoreductase; Peroxisome; Purine metabolism.
FT NON_TER
SQ SEQUENCE 8 AA; 777 MW; 98CIAD735B9D76D CRC64;

Query Match 30.6%; Score 22; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSVA 6
DB 2 PPSLA 6
ID P92386_HORMA PRELIMINARY; PRT; 8 AA.
AC P92386;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Pect protein (Fragment).
GN Name=pect;
OS Hordeum marinum subsp. gussoneanum.
OC Plantae; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP clade;
OC Pooidae; Triticeae; Hordeum.
OX NCBI_TaxID=98114;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=92721648; PubMed=9126564; DOI=10.1006/mpv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).

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DR EMBL: Z77763; CAB01368.1; -; Genomic_DNA.
DR GRAMene; P92386; -;
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 886 MW; 1EDAB8773AE735B3 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15

DB 1 KSLXLIG 6
RESULT 10
Q6EOX9_YEAST PRELIMINARY; PRT; 14 AA.
AC Q6EOX9;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Fliolp (Fragment).
GN Name=Fliol1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3238-32;
RX PubMed=15932987; DOI=10.1128/AEM.71.6.2934-2939.2005;
RA Zara S., Bakalinsky A.T., Zara G., Pirino G., Demontis M.A.,
Budroni M.,
RT "Fliol1-Based Model for Air-Liquid Interfacial Biofilm Formation by
Saccharomyces cerevisiae.";
RL Appl. Environ. Microbiol. 71:2934-2939(2005).

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DR EMBL: AY618269; AAT69750.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 14 AA; 1664 MW; 551F2C65193164D7 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 1.4e+04;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PPSVAKSVKSL 12
DB 4 PFLAYLVLSL 14
ID ASPL_LACSN STANDARD; PRT; 15 AA.
AC P82648;
DT 04-MAY-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Acid shock protein 1 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coccconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.

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KW Direct protein sequencing.
FT CHAIN 1 >15
FT NON_TER
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Acid shock protein 1.
/FTID=PRO_0000064703.

Query Match 30.6%; Score 22; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLIG 15
| | | | |
| | | | |
Db 4 KGLFLG 9

RESULT 12

P93331_STRTR PRELIMINARY; PRT; 15 AA.
ID P93331_STRTR
AC P93331;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 7.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ITG5T80;
RA Guimont C., Chopard M.A., Galliard J.L., Chamba J.F.;
RT "Comparative study of the protein composition of three strains of
RT Streptococcus thermophilus grown either in M17 medium or in milk.";
RL lait 0:0-0(2002).
CC -----
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CC -----

DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009252; P:peptidoglycan biosynthesis; IEA.
KW Cell wall; peptidoglycan synthesis.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1653 MW; 19E60997E2C4D945 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 VKSLYLIG 15
| | | | |
| | | | |
Db 1 VNSTRIG 7

RESULT 13

P92211_AGRCR PRELIMINARY; PRT; 8 AA.
ID P92211_AGRCR
AC P92211;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Peid protein (Fragment).
GN Name=peid;
OS Agropyron cristatum (Created wheatgrass).
OG Plantid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RA MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
CC -----
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CC -----
CC EMBL: Z77771; CAB01392.1; -, Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLIG 15
| | | | |
| | | | |
Db 1 KSLTLG 6

RESULT 14

P92215_9POL PRELIMINARY; PRT; 8 AA.
ID P92215_9POL
AC P92215;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Peid protein (Fragment).
GN Name=peid;
OS Amblyopyrum muticum.
OG Plantid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RA MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----

DR EMBL: Z77756; CAB01347.1; -, Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLIG 15
| | | | |
| | | | |
Db 1 KSLTLG 6

RESULT 15

P92222_BROIN PRELIMINARY; PRT; 8 AA.
ID P92222_BROIN
AC P92222;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Peid protein (Fragment).
GN Name=peid;
OS Bromus inermis (Smooth brome grass).
OG Plantid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Bromaeae; Bromus.
CC -----
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OK NCBI_TaxID=15371;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.,
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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EMBL: Z77759; CAB01356.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
|||
Db 1 KSLTLG 6

RESULT 16
P92227_CRIDE PRELIMINARY; PRT; 8 AA.
ID P92227;
AC P92227;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Crithopsis delileana.
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Crithopsis.
OX NCBI_TaxID=37674;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.,
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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EMBL: Z77751; CAB01332.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
|||
Db 1 KSLTLG 6

RESULT 17
P92373_9POAL PRELIMINARY; PRT; 8 AA.
ID P92373_9POAL

AC P92373;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Haynaldia villosa.
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.,
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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EMBL: Z77741; CAB01302.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
|||
Db 1 KSLTLG 6

RESULT 18
P92382_9POAL PRELIMINARY; PRT; 8 AA.
ID P92382;
AC P92382;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Hordeum brachyantherum.
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.,
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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EMBL: Z77761; CAB01362.1; -; Genomic_DNA.
DR Gramene; P92382; -;
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
|||
Db 1 KSLTLG 6

RESULT 19
P92382_9POAL PRELIMINARY; PRT; 8 AA.
ID P92382_9POAL

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 19

P92384_9POAL PRELIMINARY; PRT; 8 AA.
 AC P92384;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pect protein (Fragment).
 GN Name=pect;
 OS Hordeum murinum subsp. glaucum.
 OG Plantid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Hordeum.
 NCBI_TaxID=98113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77762; CAB01365.1; -; Genomic_DNA.
 DR Gramene; P92384;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 20

P92388_9POAL PRELIMINARY; PRT; 8 AA.
 AC P92388;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pect protein (Fragment).
 GN Name=pect;
 OS Henrardia perisica.
 OG Plantid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Henrardia.
 NCBI_TaxID=37678;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77750; CAB01329.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

RT sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77748; CAB01323.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 21

P92391_HETPI PRELIMINARY; PRT; 8 AA.
 AC P92391;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pect protein (Fragment).
 GN Name=pect;
 OS Heteranthellium piliferum.
 OG Plantid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Heteranthellium.
 NCBI_TaxID=37679;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77750; CAB01329.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 22

P92394_HORVU PRELIMINARY; PRT; 8 AA.
 AC P92394;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pect protein (Fragment).
 GN Name=pect;
 OS Hordeum vulgare (Barley).
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 CC -----
 CC EMBL; Z77750; CAB01329.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Hordeum.
 OX NCBI_TaxId=4513;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 DR EMBL; Z77764; CAB01371.1; -; Genomic_DNA.
 DR Gramene; P92394; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
 |||
 1 KSLTLG 6

RESULT 23
 ID P92404 LOPEL PRELIMINARY; PRT; 8 AA.
 AC P92404;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pecl protein (Fragment).
 GN Name=pecl;
 OS Lophopyrum elongatum (Tall wheatgrass) (Aragopyrum elongatum).
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Lophopyrum.
 OX NCBI_TaxId=4588;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 CC -----
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 CC -----
 DR EMBL; Z77743; CAB01308.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
 |||
 1 KSLTLG 6

RESULT 24
 ID P92422 PSAPR PRELIMINARY; PRT; 8 AA.
 AC P92422; P92420;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE Pecl protein (Fragment).
 GN Name=pecl;
 OS Psathyrostachys fragilis.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Psathyrostachys.
 OX NCBI_TaxId=37729;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 DR EMBL; Z77753; CAB01338.1; -; Genomic_DNA.
 DR EMBL; Z77752; CAB01335.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
 |||
 1 KSLTLG 6

RESULT 25
 ID P92426 PSEPI PRELIMINARY; PRT; 8 AA.
 AC P92426;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pecl protein (Fragment).
 GN Name=pecl;
 OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Aragopyron spicatum).
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Pooidae; Triticeae; Pseudoroegneria.
 OX NCBI_TaxId=4604;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 DR EMBL; Z77744; CAB01311.1; -; Genomic_DNA.

DR GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLTG 6

RESULT 26
 P92428_9POL PRELIMINARY; PRT; 8 AA.

AC P92428;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.

DE Pect protein (Fragment).
 GN Name=pect;
 OS Peridictyon sanctum.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Peridictyon.
 NCBI_TaxID=37683;

OK NCB1_TaxID=37683;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.,
 "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RT Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL; Z77749; CAB01326.1; -; Genomic_DNA.
 CC DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLTG 6

RESULT 27
 P92431_AEGTA PRELIMINARY; PRT; 8 AA.

AC P92431;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 24.

DE Pect protein (Fragment).

GN Name=pect;
 OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).

OG Plastid; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Aegilops.

OK NCB1_TaxID=37682;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.,
 "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RT Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL; Z77758; CAB01353.1; -; Genomic_DNA.
 CC DR Gramene; P92431;
 DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLTG 6

RESULT 28
 P92441_THIB PRELIMINARY; PRT; 8 AA.

AC P92441;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.

DE Pect protein (Fragment).
 GN Name=pect;
 OS Thinopyrum bessarabicum.

OG Plastid; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Thinopyrum.

NCBI_TaxID=4601;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.,
 "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."
 RT Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL; Z77769; CAB01386.1; -; Genomic_DNA.
 CC DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLTG 6

RESULT 29
 P92443_TAECM PRELIMINARY; PRT; 8 AA.

AC P92443;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Pect protein (Fragment).
GN Name=petD;
OS Taeniartherum caput-medusae (Medusaehead).
OC Placidi; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Taeniartherum.
OX NCBI_TaxId=37687;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL: Z77760; CAB01359.1; -; Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. NO. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
||| ||
Db 1 KSLTIG 6

RESULT 30
P93955 FESFE PRELIMINARY; PRT; 8 AA.
AC P93955;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 23.
DE Pect protein (Fragment).
GN Name=petD;
OS Festucopsis festuoides.
OC Placidi; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Festucopsis.
OX NCBI_TaxId=72455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL: Z77770; CAB01389.1; -; Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. NO. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
||| ||
Db 1 KSLTIG 6

RESULT 31
P93957 FESSE PRELIMINARY; PRT; 8 AA.
ID P93957;
AC P93957;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 23.
DE Pect protein (Fragment).
GN Name=petD;
OS Festucopsis sergentini.
OC Placidi; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Festucopsis.
OX NCBI_TaxId=72456;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL: Z79501; CAB01777.1; -; Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. NO. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
||| ||
Db 1 KSLTIG 6

RESULT 32
P93959 GPOAL PRELIMINARY; PRT; 8 AA.
ID P93959;
AC P93959;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 23.
DE Pect protein (Fragment).
GN Name=petD;
OS Hordeum erectifolium.
OC Placidi; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Hordeum.
OX NCBI_TaxId=58926;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----


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CC -----
CC EMBL: Z79500; CAB01776.1; -, Genomic_DNA.
DR Gramene: P93959; -.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 33
P93961 PSARU PRELIMINARY; PRT; 8 AA.
ID P93961 PSARU PRELIMINARY; PRT; 8 AA.
AC P93961;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Pept protein (Fragment).
GN Name=pept;
OS Psathyrostachys rupestris.
OC Plantid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Poideae; Triticeae; Psathyrostachys.
OX NCBI_TaxId=58938;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL: Z77755; CAB01344.1; -, Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 34
P93963 PSAST PRELIMINARY; PRT; 8 AA.
ID P93963 PSAST PRELIMINARY; PRT; 8 AA.
AC P93963;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Pept protein (Fragment).
GN Name=pept;
OS Psathyrostachys scoloniformis.
OC Plantid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

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OC Poideae; Triticeae; Psathyrostachys.
OX NCBI_TaxId=58973;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
CC -----
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CC -----
DR EMBL: Z77754; CAB01341.1; -, Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 35
P93965 SECST PRELIMINARY; PRT; 8 AA.
ID P93965 SECST PRELIMINARY; PRT; 8 AA.
AC P93965;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Pept protein (Fragment).
GN Name=pept;
OS Secale strictum.
OC Plantid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Poideae; Triticeae; Secale.
OX NCBI_TaxId=58866;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL: Z77755; CAB01373.1; -, Genomic_DNA.
DR Gramene: P93965; -.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 36

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P93966_AEGSP
ID P93966_AEGSP PRELIMINARY; PRT; 8 AA.
AC P93966;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE PeD protein (Fragment).
GN Name=peD;
OS Aegilops speltoides (Goatgrass).
OC Placidae; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BDP clade;
OC Poideae; Triticeae; Aegilops.
OX NCBI_TaxID=4573;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
-----
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-----
DR EMBL; Z77766; CAB01377.1; -; Genomic_DNA.
DR Gramene; P93966; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 83.3%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 37
P93970_9POAL PRELIMINARY; PRT; 8 AA.
ID P93970_9POAL PRELIMINARY; PRT; 8 AA.
AC P93970;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE PeD protein (Fragment).
GN Name=peD;
OS Eremopyrum triticeum.
OC Placidae; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BDP clade;
OC Poideae; Triticeae; Eremopyrum.
OX NCBI_TaxID=58937;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
-----
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-----
DR EMBL; Z77746; CAB01315.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1

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SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 83.3%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 38
P93973_EREDI PRELIMINARY; PRT; 8 AA.
ID P93973_EREDI PRELIMINARY; PRT; 8 AA.
AC P93973;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE PeD protein (Fragment).
GN Name=peD;
OS Eremopyrum distans.
OC Placidae; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BDP clade;
OC Poideae; Triticeae; Eremopyrum.
OX NCBI_TaxID=58936;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
-----
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-----
DR EMBL; Z77745; CAB01314.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 83.3%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
Db 1 KSLTLG 6

RESULT 39
P93981_9POAL PRELIMINARY; PRT; 8 AA.
ID P93981_9POAL PRELIMINARY; PRT; 8 AA.
AC P93981;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE PeD protein (Fragment).
GN Name=peD;
OS Critchodium monoccum.
OC Placidae; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BDP clade;
OC Poideae; Triticeae; Critchodium.
OX NCBI_TaxID=72428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;

```

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RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL; Z77757; CAB01350.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 1 KSLTLTG 6

RESULT 40
P33985_AEGCM PRELIMINARY; PRT; 8 AA.
ID P33985;
AC P33985;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Pecl protein (Fragment).
GN Name=pecl;
OS Aegilops comosa (Goatgrass).
OC Placrid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BCP clade;
OC Poideae; Triticeae; Aegilops.
OC NCBI_TaxID=4485;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL; Z77742; CAB01305.1; -; Genomic_DNA.
DR Gramene; P33985; -;
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 1 KSLTLTG 6

RESULT 41
P33992_AUSVE PRELIMINARY; PRT; 8 AA.
ID P33992;
AC P33992;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Pecl protein (Fragment).

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GN Name=pecl;
OS Australopyrum velutinum.
OC Placrid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BCP clade;
OC Poideae; Triticeae; Australopyrum.
OC NCBI_TaxID=58935;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL; Z77768; CAB01383.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 1 KSLTLTG 6

RESULT 42
O5EFY1_9BRYO PRELIMINARY; PRT; 9 AA.
ID O5EFY1;
AC O5EFY1;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Cytochrome b/f complex subunit IV (Fragment).
GN Name=pecl;
OS Polytichum pallidisetum.
OC Placrid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Polytichopsida; Polytichales; Polytichaceae; Polytichum.
OC NCBI_TaxID=146548;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Goffinet B.; Wickett N.J.; Shaw J.A.; Cox C.J.;
RT "Phylogenetic significance of the rpoA loss in the chloroplast genome
of mosses.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY886747; AA81785.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER
SQ SEQUENCE 9 AA; 1015 MW; 45AF287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 2 KSLTLTG 7

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RESULT 43
O5EFY7_9BRYO PRELIMINARY; PRT; 9 AA.
AC O5EFY7;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Cytochrome b/f complex subunit IV (Fragment).
GN Name=petd;
OS Oedipodium griffithianum.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Polytrophicopsida; Tetraraphales; Oedipodiaceae; Oedipodium.
OX NCBI_TaxID=127538;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
RT "Phylogenetic significance of the rpoa loss in the chloroplast genome
of mosses."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AY866744; AAM81777.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 9 AA; 993 MW; 4A93287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
DB 2 KSLYLG 7

RESULT 44
O5EFZ0_9BRYO PRELIMINARY; PRT; 9 AA.
AC O5EFZ0;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Cytochrome b/f complex subunit IV (Fragment).
GN Name=petd;
OS Buxbaumia aphylla.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Polytrophicopsida; Tetraraphales; Buxbaumiaceae; Buxbaumia.
OX NCBI_TaxID=70128;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
RT "Phylogenetic significance of the rpoa loss in the chloroplast genome
of mosses."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AY866743; AAM81774.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 9 AA; 993 MW; 4A93287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 10 KSLYLG 15
DB 2 KSLYLG 7

RESULT 45
O3YLMB_STRAB PRELIMINARY; PRT; 10 AA.
AC O3YLMB;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE NADH dehydrogenase subunit 6 (Fragment).
OS Strix aluco sylvatica.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Strix.
OX NCBI_TaxID=340960;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Brito P.H.;
RT "The influence of Pleistocene glacial refugia on tawny owl genetic
diversity and phylogeography in western Europe."
RL Mol. Ecol. 14:3077-3094(2005).
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-----
DR EMBL; DQ087079; AAZ77348.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 10 AA; 1238 MW; 1F934E3B572699DB CRC64;

Query Match 29.2%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.15e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LYLIG 15
DB 6 LYLIG 9

RESULT 46
O31851_ARATH PRELIMINARY; PRT; 12 AA.
AC O31851;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Columbia; TISSUE=Leaf;
RX MEDLINE=94187724; PubMed=8139595;
RA Conley T.R., Park S.-C., Kwon H.-B., Peng H.-S., Shih M.-C.;
RT "Characterization of cis-acting elements in light regulation of the
nuclear gene encoding the A subunit of chloroplast isozymes
glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana."
RL Mol. Cell. Biol. 14:2525-2533(1994).
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-----
DR EMBL; U14743; AAA31640.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
```

DR GO:0005634; C:nucleus; IEA.
KW Chloroplast; Nuclear protein.
FT NON TER 12
SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.8e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 VPFSVAK 7
| | | | |
Db 4 VTFSVVK 10

RESULT 47
071475_9CRYP PRELIMINARY; PRT; 14 AA.
AC 071475;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE tRNA proteolysis tag (Fragment).
GN Name=serA; Rhodomonas salina.
OS Rhodomonas salina.
OG Plastid.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP1319;
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Guenau de Nova P., Williams K.P.;
RT "The tRNA website: reductive evolution of tRNA in plastids and other endosymbionts";
RL Nucleic Acids Res. 32:D104-D108(2004).
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CC
DR EMBL; AF550355; AAQ12671.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFS 4
| | | |
Db 5 VPFS 8

RESULT 48
085662_REOVJ PRELIMINARY; PRT; 14 AA.
AC 085662;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE Reovirus serotype 2 S2 (Fragment).
OS Reovirus type 2 (strain D5/Jones) (T2J) (Mammalian orthoreovirus 2).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83017877; PubMed=7123853;
RA Galliard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus serotypes";
RL Virology 121:320-326(1982).
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CC
DR EMBL; J02311; AAA47250.1; -; Genomic_RNA.
FT NON TER 14
SQ SEQUENCE 14 AA; 1459 MW; 03FA0D6A8B9A30 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.1e+04;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 6 AKSVKSLYL 14
| : | : | : |
Db 4 ARSITVGL 12

RESULT 49
09UCC2_HUMAN PRELIMINARY; PRT; 15 AA.
AC 09UCC2;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE 35 kDa heparin-RELEASABLE protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the cytokines midline and pleiotrophin, in human postheparin plasma";
RL Arterioscler. Thromb. 13:1798-1805(1993).
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CC
SQ SEQUENCE 15 AA; 1456 MW; 0585F6F4F8F6265 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.3e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKS 9
| | : | : | : |
Db 6 VPIPLXKSL 14

RESULT 50
04X416_PLACH PRELIMINARY; PRT; 15 AA.
AC 04X416;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC400385.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karim M., Raine J.D., Carleton J.M., Kooij T.W.A.,
RA Beriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Oualil M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses";

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RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: CAJ01010035; CAH88301.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1735 MW; 9525B601566669C CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLYL 14
DB 4 AKPISISYI 12

RESULT 51
ID Q714TB_9FLOR PRELIMINARY; PRT; 15 AA.
AC Q714TB;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE tRNA proteolysis tag (Fragment).
GN Name=sra;
OS Masticarpus papillatus.
OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Petrocelidaceae;
OC Macrocarpus.
CC NCBI_TaxID=31436;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Guenau de Nova P., Williams K.P.;
RT "The tRNA website: reductive evolution of tRNA in plastids and other
RT endosymbionts."
RL Nucleic Acids Res. 32:DI04-DI08(2004).
CC -----
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CC -----
DR EMBL: AF550352; AAQ12668.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1735 MW; D98014394A33D2BC CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
DB 6 VPFS 9

RESULT 52
ID Q7S5J5_NEUCR PRELIMINARY; PRT; 10 AA.
AC Q7S5J5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Predicted protein.
GN ORFNames=NCU06092.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
CC NCBI_TaxID=5141;

```

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RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccelli S., Rehman B.,
RA Ekins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Mashburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staeben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamysseilis M.,
RA Mauceli E., Bielke C., Rudd S., Fishman D., Krystofova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Carcheside D.E.A., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Veilker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannheim G., Ebbole D.J., Freltag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa."
RL Nature 422:859-868(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL: AABX01000354; EAA30718.1; -; Genomic_DNA.
SQ SEQUENCE 10 AA; 1224 MW; 4C43FE232411B1A3 CRC64;

Query Match
Best Local Similarity 27.8%; Score 20; DB 2; Length 10;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 VAKSVKSLY 13
DB 1 MAKTTRKLF 9

RESULT 53
ID P83161_ANASL PRELIMINARY; PRT; 10 AA.
AC P83161;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative RNA-binding protein rtpa (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
CC NCBI_TaxID=29412;
RN [1]
RP PROTEIN SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Alendort K.;
RL Submitted (OCT-2001) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -----
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CC -----
DR GO: 0003723; F:RNA binding; IEA.
DR InterPro: IPR000504; RNP1_RNA_bd.
KW RNA-binding.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1130 MW; 1DD09AB7244862DB CRC64;

Query Match
Best Local Similarity 27.8%; Score 20; DB 2; Length 10;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLVIG 15
DB 1 SLVIG 5

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```

RESULT 54
053VR5_MOUSE PRELIMINARY; PRT; 11 AA.
ID 053VR5_MOUSE
AC 053VR5;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE D region (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=66136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBL J. 4:3681-3688(1985).
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-----
DR EMBL; X03375; CAA27081.1; -; mRNA.
DR EMBL; X03374; CAA27075.1; -; mRNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1318 MW; CLE17837587AB5B9 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
Db 2 IPFS 5

RESULT 55
086866_9VIRU PRELIMINARY; PRT; 11 AA.
ID 086866_9VIRU
AC 086866;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE S-RNA product protein (Fragment).
DE Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
choriomeningitis virus.";
J. Virol. 69:2187-2193(1995).
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-----
DR EMBL; S75748; AAB33668.1; -; mRNA.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1200 MW; 54235C80D9C45B57 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 9 VKSLY 13
Db 1 IKALY 5

RESULT 56
086868_9VIRU PRELIMINARY; PRT; 11 AA.
ID 086868_9VIRU
AC 086868;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE S-RNA product protein (Fragment).
DE Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
choriomeningitis virus.";
J. Virol. 69:2187-2193(1995).
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-----
DR EMBL; S75751; AAB33671.1; -; mRNA.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1200 MW; 54235C80D9C45B57 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 VKSLY 13
Db 1 IKALY 5

RESULT 57
HCYB_MEGCR STANDARD; PRT; 12 AA.
ID HCYB_MEGCR
AC 010584;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Hemocyanin B chain (KLH-B) (Fragment).
DE Megathura crenulata (Giant keyhole limpet).
OS Megathura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Fissurellidae; Fissurellidae; Megathura.
NCBI_TaxID=55429;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96208935; PubMed=8829804; DOI=10.1016/0305-0491(95)02091-8;
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional characterization
of two different subunits and multimers.";
Comp. Biochem. Physiol. 113B:537-548(1996).
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CC Occurring freely dissolved in the hemolymph of many mollusks and
arthropods.
CC -1- SUBUNIT: Dodecamers and extended multimers.
CC -1- SUBCELLULAR LOCATION: Secreted protein; extracellular space.
CC -1- TISSUE SPECIFICITY: Hemolymph.
CC -1- BIOTECHNOLOGY: Potent immunogen used classically as a carrier
protein for haptens and more recently in human vaccines and for
immunotherapy of bladder cancer.
CC -1- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
subfamily.

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CC -----
DR InterPro; IPR000896; Hemocyanin.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
DR Copper; Direct protein sequencing; Hemolymph; Oxygen transport;
KW Transport.
FT CHAIN 1 >12 Hemocyanin B chain.
FT FTId=PRO_0000204305.
SQ SEQUENCE 12 AA; 1345 MW; CBFBEAA44A32412 CRC64;
Query Match
Best Local Similarity 27.8%; Score 20; DB 1; Length 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 VAKSVKSL 12
DB 5 VAKNVDSL 12
RESULT 58
Q945C3_CRYCO PRELIMINARY; PRT; 12 AA.
AC Q945C3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE P80 protein (Fragment).
OS Cryptocodium cohnii (Dinoflagellate).
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptecodiniaceae;
OC Cryptecodinium.
OX NCBI_TaxID=2866;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9943338; PubMed=10505419;
RA Ausseil J., Soyer-Gobillard M.O., Geraud M.L., Bhaud Y., Baines I.,
RA Preston T., Moreau H.;
RT "Characterization of p80, a novel nuclear and cytoplasmic protein in
RT dinoflagellates.",
RL Proclst 150:197-211(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21428164; PubMed=11545436;
RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;
RT "Role of nuclear MW domains and proline-rich proteins in
RT dinoflagellate transcription.",
RL Proclst 152:127-138(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22287324; PubMed=12154093; DOI=10.1074/jbc.M205624200;
RA Guillebaud D., Sasorith S., Derelle E., Wurtz J.M., Lozano J.C.,
RA Bingham S., Tora L., Moreau H.;
RT "A new class of transcription initiation factors, intermediate between
RT TATA box-binding proteins (TBP) and TBP-like factors (TLFPs), is
RT present in the marine unicellular organism, the dinoflagellate
RT Cryptocodium cohnii.",
RL J. Biol. Chem. 277:40881-40886(2002).
CC -----
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CC -----
DR EMBL; AF415568; AAL15906.1; -, Genomic_DNA.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1364 MW; 615BF873FE204414 CRC64;
Query Match
Best Local Similarity 27.8%; Score 20; DB 2; Length 12;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 5 VAKSVKSLYLG 15

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DB 1 MASARRLFIG 11
RESULT 59
Q6VSD4_9LABR PRELIMINARY; PRT; 12 AA.
AC Q6VSD4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Ribosomal protein S7 (Fragment).
OS Thalassoma sanctaehelenae.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC Labridae; Thalassoma.
OX NCBI_TaxID=239036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bernardi G., Bucciarelli G., Costagliola D., Robertson R.,
RA Heiser J.B.;
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY328665; AAQ86984.1; -, Genomic_DNA.
RX GO:0003735; Functional constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1310 MW; 02163AA3F9533DD4 CRC64;
Query Match
Best Local Similarity 27.8%; Score 20; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AKSVKS 11
DB 6 AKIVKS 11
RESULT 60
UPE71_LITZW
ID UPE71_LITZW STANDARD; PRT; 13 AA.
AC P82050;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, entry version 1.
DE Uperlin-7.1 [Contains: Uperlin-7.1.1].
OS Litorea ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litorea.
OX NCBI_TaxID=104896;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RA Steinborner S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combination of peptides from the skin glands of Ewing's
RT tree frog, Litorea ewingi. Sequence determination and antimicrobial
RT activity.",
RL Aust. J. Chem. 50:889-894(1997).
CC -!- FUNCTION: Uperlin 7.1 shows antibacterial activity against L.lactis
CC and S.uberis. Uperlin 7.1.1 is inactive.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1427; METHOD=FAE; RANGE=1-13; NOTE=Ref.1.
CC -!- MASS SPECTROMETRY: MW=1184; METHOD=FAE; RANGE=1-13; NOTE=Ref.1.
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CC -----

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KW Amidation; Amphibian defense peptide; Antibiotic; Antimicrobial;
KM Direct protein sequencing.
FT PEPTIDE 1 13 Uperin-7.1.
FT PEPTIDE 3 13 /FTId=PRO_0000010302.
FT PEPTIDE 3 13 Uperin-7.1.1.
FT MOD RES 13 13 /FTId=PRO_0000010303.
FT MOD RES 13 13 Valine amide.
SQ SEQUENCE 13 AA; 1429 MW; D617C7204CCAE322 CRC64;
Query Match 27.8%; Score 20; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 3e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 FSVAKSVKS 11
DB 3 FDVVKHIAS 11
RESULT 61
Q14461 HUMAN PRELIMINARY; PRT; 13 AA.
AC Q14461_Q14842; Integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Glycophorin B (Fragment).
GN Name=GYPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90264417; PubMed=1971625;
RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
RT "Identification of the crossing-over point of a hybrid gene encoding human glycoprotein variant Sta. Similarity to the crossing-over point in haploglobin-related genes."
RT J. Biol. Chem. 265:9259-9263(1990).
RL J. Biol. Chem. 265:9259-9263(1990).
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CC -----
DR EMBL: M33505; AA53152.1; -, Genomic_DNA.
DR PIR: I70075; I70075.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1565 MW; 466944F750D145B7 CRC64;
Query Match 27.8%; Score 20; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 SVKSLV 13
DB 7 SIYSIV 12
RESULT 62
BRK3 RANNI STANDARD; PRT; 14 AA.
AC Q7L253;
DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Bradykinin-like peptide 3.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
OC Pelophylax.
OX NCBI_TaxID=8409;
RN [1]
RP PROTEIN SEQUENCE.

RC TISSUE=Skin;
RX MEDLINE=69117202; PubMed=5751736;
RA Nakajima T.;
RT "On the third active peptide on smooth muscle in the skin of Rana nigromaculata hallowell.";
RL Chem. Pharm. Bull. 16:2088-2089(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: secreted protein.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
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CC -----
DR PIR: A61362; A61362.
KM Direct protein sequencing; Vasoactive; Vasodilator.
FT PEPTIDE 1 14 Bradykinin-like peptide 3.
FT SEQUENCE 14 AA; 1486 MW; 33344EB3978393D7 CRC64;
Query Match 27.8%; Score 20; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 3.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PFSVA 6
DB 7 PFRVA 11
RESULT 63
HCYA MEGCR
ID HCYA_MEGCR STANDARD; PRT; 14 AA.
AC Q10583;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Hemocyanin A chain (KLM-A) (Fragment).
OS Megachura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orchoastropoda;
OC Veligasteropoda; Fissurellioidea; Fissurellidae; Megachura.
OX NCBI_TaxID=55429;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96208935; PubMed=8229804; DOI=10.1016/0305-0491(95)02091-8;
RA Smerlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "keyhole limpet hemocyanin: structural and functional characterization of two different subunits and multimers."
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -1- FUNCTION: Hemocyanins are copper-containing oxygen carriers occurring freely dissolved in the hemolymph of many mollusks and arthropods.
CC -1- SUBUNIT: Decamers and didecamers.
CC -1- SUBCELLULAR LOCATION: Secreted protein; extracellular space.
CC -1- TISSUE SPECIFICITY: Hemolymph.
CC -1- BIOTECHNOLOGY: Potent immunogen used classically as a carrier protein for haptens and more recently in human vaccines and for immunotherapy of bladder cancer.
CC -1- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin subfamily.
CC -----
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CC -----
DR InterPro: IPR000896; Hemocyanin.
DR PROSITE: PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE: PS00210; HEMOCYANIN_2; PARTIAL.
KM Copper; Direct protein sequencing; Hemolymph; Oxygen transport; Transport.
FT CHAIN 1 >14 Hemocyanin A chain.
FT NON_TER 14 14 /FTId=PRO_0000204304.
SQ SEQUENCE 14 AA; 1610 MW; 9CE61977014A99D5 CRC64;
Query Match 27.8%; Score 20; DB 1; Length 14;

Best Local Similarity 62.5%; Pred. No. 3.2e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 VAKSVKSL 12
| | | | |
Db 4 VAKSVKSL 11

RESULT 64

096050 HUMAN PRELIMINARY; PRT; 14 AA.

AC 096050; Integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Mitochondrial ribosomal protein L33 (Fragment).

GN Name=MRL33;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=21429115; PubMed=11543634; DOI=10.1006/geno.2001.6622;

RA Katoch N., Suzuki T., Uechi T., Magoor M., Kuniba M., Higa S.,

RA Watanabe K., Tanaka T.,

RT "The human mitochondrial ribosomal protein genes: mapping of 54 genes

to the chromosomes and implications for human disorders.";

RL Genomics 77:65-70(2001).

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CC EMBL; AB051623; BAB54951.1; -; Genomic DNA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

KM Ribosomal protein.

FT NON_TER 1 1

SQ SEQUENCE 14 AA; 1744 MW; 64ED243B9AED63B CRC64;

Query Match 27.8%; Score 20; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 3.2e+04;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 VPSVAVKSVKSL 12

| | | | |

Db 3 VLFVEKKKIRSL 14

RESULT 65

0382J5 LACSS PRELIMINARY; PRT; 15 AA.

AC 0382J5; Integrated into UniProtKB/TrEMBL.

DT 22-NOV-2005, sequence version 1.

DT 07-MAR-2006, entry version 4.

DE Hypothetical small peptide.

GN OrderedLocustNames=LSA0083;

OS Lactobacillus sakei subsp. sakei (strain 23K).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI_TaxID=314315;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA PubMed=16273110; DOI=10.1038/nbt1160;

RA Chailion S., Champomier-Verges M.-C., Cornet M., Cruz-Le Cog A.-M.,

RA Duder A.-M., Martin V., Beaufils S., Darbon-Rongere E., Bossy R.,

RA Loux V., Zagorec M.,

RT "The complete genome sequence of the meat-borne lactic acid bacterium

Lactobacillus sakei 23K.";

RL Nat. Biotechnol. 23:1527-1533 (2005).

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CC EMBL; CR936503; CA154382.1; -; Genomic DNA.

DR GenomeReviews; CR936503.GR; LSA0083.

KM Complete proteome; Hypothetical protein.

SQ SEQUENCE 15 AA; 1676 MW; 95F386574D90FEB3 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 3.5e+04;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 SVKSVKSL 13

| | | | |

Db 2 SVKSVKSL 11

RESULT 66

070Y88 GLAMI PRELIMINARY; PRT; 8 AA.

AC 070Y88; Integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 8.

DE Ribosomal protein (Fragment).

GN Name=Ips16;

OS Placostoma fimbriatum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae;

OC Placostoma.

OX NCBI_TaxID=204168;

RP NUCLEOTIDE SEQUENCE.

RA PubMed=15019625; DOI=10.1016/j.ympv.2003.08.002;

RA Paton A., Springate D.A., Sude S., Otiemo D., Grayer R., Harley M.M.,

RA Willis F., Simonds M.S., Powell M.P., Savolainen V.,

RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)

based on three plastid DNA regions.";

RL Mol. Phylogenet. Evol. 31:277-299(2004).

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CC EMBL; AJ505368; CAD45489.1; -; Genomic DNA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

KM Ribosomal protein.

FT NON_TER 1 1

SQ SEQUENCE 8 AA; 789 MW; 86786772D1B4772 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 8;

Best Local Similarity 60.0%; Pred. No. 2.8e+06;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPSV 5

| | | | |

Db 1 VPSV 5

RESULT 67

06UIQ3 MACMU PRELIMINARY; PRT; 9 AA.

AC 06UIQ3; Integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 6.

DE Glutamine-fructose-6-phosphate transaminase 1 (Fragment).

GN Name=GFPT1;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecoidea; Cercopithecinae; Macaca.

OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22946167; PubMed=14557539; DOI=10.1073/pnas.2135499100;
 RA Caceres M., Lachner J., Zapala M.A., Redmond J.C., Kudo L.,
 RA Geschwind D.H., Lockhart D.J., Preuss T.M., Barlow C.,
 RT "Elevated gene expression levels distinguish human from non-human
 RT primate brains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:13030-13035(2003).
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 CC -----
 DR EMBL: AY369811; AAR11242.1; -; mRNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 960 MW; 5BF4D1B2D5B33DD7 CRC64;
 Query Match 26.4%; Score 19; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SVAKSV 9
 Db 1 NLAHSV 6
 RESULT 68
 ID Q607P3_RALEU PRELIMINARY; PRT; 9 AA.
 AC Q607P3;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Glucosamine synthetase (Fragment).
 GN Name=glms;
 OS Ralstonia eutropha (Alcaligenes eutrophus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Cupriavidus.
 OX NCBI_TaxID=106590;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Aspary T.J., Burns R.G.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AY553854; AAS6992.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 960 MW; 5BF4D1B2D5B33DD7 CRC64;
 Query Match 26.4%; Score 19; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SVAKSV 9
 Db 1 NLAHSV 6
 RESULT 69
 ID Q476S1_ECOLI PRELIMINARY; PRT; 10 AA.
 AC Q476S1;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE TrpA protein (Fragment).
 GN Name=trpA;
 OS Escherichia coli.
 OC Bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=88118903; PubMed=3323526;
 RA Jalajakumari M.B., Guidolin A., Buhj H.J., Manning P.A.;
 RT "Surface exclusion genes trsA and trsB of the F sex factor of
 RT Escherichia coli K-12. Determination of the nucleotide sequence and
 RT promoter and terminator activities.";
 RL J. Mol. Biol. 198:1-11(1987).
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 CC -----
 DR EMBL: D90177; BAA14207.1; -; Genomic_DNA.
 KM Plasmid.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1070 MW; CCI8014DD045B33D CRC64;
 Query Match 26.4%; Score 19; DB 2; Length 10;
 Best Local Similarity 37.5%; Pred. No. 3.5e+04;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 5 VAKSVKSL 12
 Db 2 LAKSIANI 9
 RESULT 70
 ID Q9UCP2_HUMAN PRELIMINARY; PRT; 11 AA.
 AC Q9UCP2;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE cGMP-inhibited LOM K(M) cAMP phosphodiesterase PEAK 43, CGI-PDE
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92283180; PubMed=1317779; DOI=10.1210/en.130.6.3265;
 RA Lebon T.R., Kaenya J., Paxton R.J., Belfrage P., Hockman S.,
 RA Manganiello V.C., Fujita Yamaguchi Y.;
 RT "Purification and characterization of guanosine 3',5'-monophosphate-
 RT inhibited low K(M) adenosine 3',5'-monophosphate phosphodiesterase
 RT from human placental cytosolic fractions.";
 RL Endocrinology 130:3265-3274(1992).
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 CC -----
 DR GO: GO:0005829; Cytosol; TAS.
 DR GO: GO:0004115; FcAMP-specific phosphodiesterase activity; TAS.
 DR GO: GO:0007165; P signal transduction; NAS.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1220 MW; 7DF1PDFD44735BB CRC64;
 Query Match 26.4%; Score 19; DB 2; Length 11;
 Best Local Similarity 27.3%; Pred. No. 3.8e+04;

Matches 3; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
|:|:|:|:
Db 1 SINESLINALFI 11

RESULT 71
059AX1 9COL PRELIMINARY; PRT; 11 AA.
AC 059AX1
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE NADH dehydrogenase subunit 1 (Fragment).
GN Name=NADH1;
OS Cicindela (Rivacindela) sp. JP-36.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Adephaga; Cicindelidae;
OC Cicindela; Rivacindela.
OX NCBI_TaxID=258626;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=36_4;
RX PubMed=15647517; DOI=10.1093/molbev/msi085;
RA Pons J., Vogler A.;
RT "Complex Pattern of Coalescence and Fast Evolution of a Mitochondrial
rRNA Pseudogene in a Recent Radiation of Tiger Beetles";
RL Mol. Biol. Evol. 22:991-1000(2005).
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CC
DR EMBL; AJ619231; CAG18254.1; -; Genomic_DNA.
DR GO; GO:0005739; Mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 11
SO SEQUENCE 11 AA; 1283 MW; 220384AE27272AA8 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LYLG 15
|:|:|:
Db 1 MYLG 4

RESULT 72
05UIX7 9FLOR PRELIMINARY; PRT; 12 AA.
AC 05UIX7
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Cytochrome oxidase subunit 3 (Fragment).
OS Gracilaria vermiculophylla.
OC Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae;
OC Gracilaria.
OX NCBI_TaxID=257814;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ruess J.;
RT "Life history and molecular sequences of Gracilaria vermiculophylla
(Gracilariaceae, Rhodophyta), a new introduction to European waters.";
RL Phycologia 0:0-0(2005).
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CC
DR EMBL; AY725143; AAV51349.1; -; Genomic_DNA.

DR GO; GO:0005739; Mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 12
SO SEQUENCE 12 AA; 1383 MW; 87F0F2C11CA2D6C5 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.2e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VAKSVK 10
|:|:|:|:
Db 7 VAKSVQ 12

RESULT 73
06PAJ9 MOUSE PRELIMINARY; PRT; 12 AA.
AC 06PAJ9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 11.
DE D11WSu47e protein.
GN Name=D11WSu47e;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uedl T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strussberg R.;
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; BC060257; AAH60257.1; -; mRNA.
DR MGI; MGI:106356; D11WSu47e.
SO SEQUENCE 12 AA; 1262 MW; DFEA9D95A4D33DC2 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.2e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SVAKSV 9
|:|:|:|:
Db 4 SVAKAM 9

RESULT 74
 DAH11_LITDA STANDARD; PRT; 13 AA.
 AC P84273;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 23-NOV-2004, sequence version 1.
 DE Dahlein-1.1.
 OS Litoria dahlii (Dahl's aquatic frog).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
 OC Pelodytidae; Litoria.
 OX NCBI_TaxID=299727;
 RN [1]
 RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
 AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX PubMed=11555873; DOI=10.1002/rcm.429;
 RA Wegener K.L., Brinkworth C.S., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Bioactive dahelein peptides from the skin secretions of the Australian
 aquatic frog Litoria dahlii: sequence determination by electrospray
 mass spectrometry.";
 RT Rapid Commun. Mass Spectrom. 15:1726-1734(2001).
 RL -1- FUNCTION: Weak wide spectrum antimicrobial activity against Gram-
 positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -1- MASS SPECTROMETRY: MW=1430; METHOD=Electrospray; RANGE=1-13;
 CC NOTE=Ref.1.

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 DR GO:0005576; C:extracellular region; IDA.
 DR GO:0050830; P:defense response to Gram-positive bacteria; IDA.
 DR InterPro: IPR013157; Antimicrobial_20.
 DR Pfam: PF08256; Antimicrobial20; 1.
 DR Amphibian defense peptide; Antibiocic; Antimicrobial;
 KW Direct protein sequencing.
 FT PEPTIDE 1 13 Dahlein-1.1.
 FT /FTID=PRO_0000043772.
 FT /FTID=8722BECF330 CRC64;
 SQ SEQUENCE 13 AA; 1433 MW; 10488722BECF330 CRC64;
 Query Match 26.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 4.6e+04;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 3 PSVAKSVKS 11
 DB 3 FDIKNIVS 11

 RESULT 75
 SAH11_POPEU STANDARD; PRT; 13 AA.
 AC P84533;
 DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUN-2005, sequence version 1.
 DE Adenosylhomocysteinease 1 (EC 3.3.1.1) (S-adenosyl-L-homocysteine
 hydrolase) (AdoHcyase) (Fragment).
 OS Populus euphratica (Euphrates poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eustosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 OX NCBI_TaxID=75702;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=leaf;
 RA Ferreira S., Hjerno K., Larsen M., Wingsle G., Larsen P., Fey S.,
 RA Roepstorff P., Pals M.S.;
 RT "Proteome profiling of Populus euphratica Oliv. upon heat stress.";
 RT Submitted (APR-2005) to Swiss-Prot.

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RL Submitted (APR-2005) to Swiss-Prot.
 CC -1- FUNCTION: Adenosylhomocysteine is a competitive inhibitor of S-
 CC adenosyl-L-methionine-dependent methyl transferase reactions;
 CC therefore adenosylhomocysteine may play a key role in the
 CC control of methylations via regulation of the intracellular
 CC concentration of adenosylhomocysteine (By similarity).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
 CC -----
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 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR PROSITE: PS00738; ADOHCYASE_1; PARTIAL.
 DR PROSITE: PS00739; ADOHCYASE_2; PARTIAL.
 KW Direct protein sequencing; Hydrolase; NAD; One-carbon metabolism.
 FT CHAIN <1 >13 Adenosylhomocysteinease 1.
 FT /FTID=PRO_0000116930.
 FT NON TER 1 1
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1394 MW; 897A15F868D376C5 CRC64;
 Query Match 26.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 4.6e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 2 PSVAK 7
 DB 8 PFKGAK 13

 RESULT 76
 SAH12_POPEU STANDARD; PRT; 13 AA.
 AC P84532;
 DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUN-2005, sequence version 1.
 DE Adenosylhomocysteinease 2 (EC 3.3.1.1) (S-adenosyl-L-homocysteine
 hydrolase) (AdoHcyase) (Fragment).
 OS Populus euphratica (Euphrates poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eustosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 OX NCBI_TaxID=75702;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=leaf;
 RA Ferreira S., Hjerno K., Larsen M., Wingsle G., Larsen P., Fey S.,
 RA Roepstorff P., Pals M.S.;
 RT "Proteome profiling of Populus euphratica Oliv. upon heat stress.";
 RT Submitted (APR-2005) to Swiss-Prot.

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 CC -1- FUNCTION: Adenosylhomocysteine is a competitive inhibitor of S-
 CC adenosyl-L-methionine-dependent methyl transferase reactions;
 CC therefore adenosylhomocysteine may play a key role in the
 CC control of methylations via regulation of the intracellular
 CC concentration of adenosylhomocysteine (By similarity).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
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 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR PROSITE: PS00738; ADOHCYASE_1; PARTIAL.
 DR PROSITE: PS00739; ADOHCYASE_2; PARTIAL.

DR PROSITE, PS00739; ADOHCYASE_2; PARTIAL.
KM Direct protein sequencing; Hydrolase; NAD; One-carbon metabolism.
FT CHAIN <1 >13 Adenosylhomocysteinease 2.
FT NON_TER 1 1 /FTid=PRO_0000116911.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1364 MW; 897A15F878D276C5 CRC64;
Query Match 26.4%; Score 19; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PPSVAK 7
DB 8 PFKGAK 13
RESULT 77
ID 097122_TOXGO PRELIMINARY; PRT; 13 AA.
AC 097122;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DE 07-FEB-2006, entry version 11.
DE Ycf24 protein (Fragment).
OS Name=ycf24;
OC Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OC NCBI_TaxID=5811;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RH;
RA Aiello D.P., Lang-Unnasch N.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AF095904; AADI7841.1; -; Genomic_DNA.
DR NON_TER 1 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FDC040D CRC64;
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DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 11.
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OS Name=ycf24;
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OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
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RC STRAIN=NC1;
RA MEDLINE=20074141; PubMed=16084442; DOI=10.1016/S0020-7519(99)00119-8;
RA Lang-Unnasch N., Aiello D.P.;
RT "Sequence evidence for an altered genetic code in the Neospora caninum
RT plasmid."
RL Int. J. Parasitol. 29:1557-1562(1999).

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CC EMBL; AF138960; AAF14260.1; -; Genomic_DNA.
DR NON_TER 1 1
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DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 14.
DE U22661.
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OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Robison K.;
RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,

RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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Query Match 26.4%; Score 19; DB 2; Length 14;
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Search completed: July 12, 2006, 05:39:16
Job time : 317 secs

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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:51:00 ; Search time 174 Seconds
(without alignments)
39.932 Million cell updates/sec

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Perfect score: 72
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 800 summaries

Database : Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	38.9	7	US-10-820-067A-361	Sequence 361, App
3	28	38.9	8	US-10-776-521B-152	Sequence 152, App
4	28	38.9	8	US-10-820-067A-648	Sequence 648, App
5	27	37.5	15	US-10-943-793-17	Sequence 17, App
6	26	36.1	11	US-09-852-910-81	Sequence 81, App
7	26	36.1	11	US-10-411-336A-81	Sequence 81, App
8	26	36.1	12	US-09-563-222-35	Sequence 35, App
9	26	36.1	12	US-10-461-878-1	Sequence 1, App
10	26	36.1	12	US-10-783-950-35	Sequence 35, App
11	26	36.1	12	US-10-461-885-1	Sequence 1, App
12	26	36.1	12	US-10-507-662-11	Sequence 11, App
13	26	36.1	14	US-09-820-649-519	Sequence 519, App
14	26	36.1	14	US-10-160-162-319	Sequence 319, App
15	26	36.1	14	US-10-936-773-319	Sequence 319, App
16	26	36.1	15	US-09-907-969-500	Sequence 500, App
17	26	36.1	15	US-10-198-053-500	Sequence 500, App
18	26	36.1	15	US-10-431-096-289	Sequence 289, App
19	26	36.1	15	US-10-860-790-500	Sequence 500, App
20	25.5	35.4	14	US-10-676-909-53	Sequence 53, App
21	25.5	35.4	15	US-10-676-909-54	Sequence 54, App
22	25	34.7	8	US-09-920-480B-9	Sequence 9, App
23	25	34.7	8	US-10-333-430-17	Sequence 17, App
24	25	34.7	9	US-09-847-185-30	Sequence 30, App
25	25	34.7	9	US-09-862-260A-3	Sequence 3, App
26	25	34.7	9	US-09-862-260A-23	Sequence 23, App
27	25	34.7	9	US-09-923-831-31	Sequence 31, App

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109	25	34.7	9	4	US-10-685-977-95	Sequence 95, Appl	182	24	33.3	13	4	US-10-234-671-60	Sequence 129, App
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160	24	33.3	9	3	US-09-935-682-22	Sequence 22, Appl	233	23	31.9	12	5	US-10-891-658-113	Sequence 113, App
161	24	33.3	9	4	US-10-119-536A-41	Sequence 41, Appl	234	23	31.9	12	5	US-10-891-658-125	Sequence 125, App
162	24	33.3	9	5	US-10-996-306-41	Sequence 41, Appl	235	23	31.9	12	5	US-10-891-658-135	Sequence 135, App
163	24	33.3	9	6	US-11-018-868-131	Sequence 131, App	236	23	31.9	12	5	US-10-630-009-41	Sequence 41, Appl
164	24	33.3	10	3	US-09-779-308-267	Sequence 267, App	237	23	31.9	12	5	US-10-630-009-41	Sequence 41, Appl
165	24	33.3	10	3	US-09-779-308-337	Sequence 337, App	238	23	31.9	12	5	US-10-630-009-41	Sequence 41, Appl
166	24	33.3	10	3	US-09-779-308-567	Sequence 567, App	239	23	31.9	12	5	US-10-630-009-42	Sequence 42, Appl
167	24	33.3	10	3	US-09-779-308-637	Sequence 637, App	240	23	31.9	12	5	US-10-506-743-4	Sequence 4, Appl1
168	24	33.3	10	3	US-09-572-404B-1725	Sequence 1725, Ap	241	23	31.9	12	5	US-10-982-725-8	Sequence 8, Appl1
169	24	33.3	10	3	US-09-573-822C-212	Sequence 212, App	242	23	31.9	12	5	US-10-505-313-96	Sequence 96, Appl
170	24	33.3	10	3	US-09-573-822C-481	Sequence 481, App	243	23	31.9	12	5	US-10-505-313-143	Sequence 143, App
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173	24	33.3	11	5	US-10-839-525-127	Sequence 127, App	246	23	31.9	12	5	US-10-507-662-12	Sequence 12, Appl

247	23	31.9	12	5	US-10-850-635-10	Sequence 30, Appl	320	22	30.6	10	4	US-10-481-180-776	Sequence 776, App
248	23	31.9	12	5	US-10-850-635-36	Sequence 36, Appl	321	22	30.6	10	4	US-10-243-795-972	Sequence 972, App
249	23	31.9	12	5	US-10-880-238-84	Sequence 84, Appl	322	22	30.6	10	4	US-10-243-795-1635	Sequence 1635, App
250	23	31.9	12	5	US-10-880-238-87	Sequence 87, Appl	323	22	30.6	10	5	US-10-474-860A-266	Sequence 266, App
251	23	31.9	12	5	US-10-880-238-90	Sequence 90, Appl	324	22	30.6	10	5	US-10-846-548A-6	Sequence 6, Appl1
252	23	31.9	12	5	US-10-880-238-93	Sequence 93, Appl	325	22	30.6	10	6	US-11-029-311-43	Sequence 43, Appl
253	23	31.9	12	5	US-10-880-238-96	Sequence 96, Appl	326	22	30.6	10	6	US-11-045-024-81	Sequence 81, Appl
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257	23	31.9	12	6	US-11-009-731-53	Sequence 53, App	330	22	30.6	11	5	US-10-807-807-1620	Sequence 1620, App
258	23	31.9	12	6	US-11-009-731-55	Sequence 55, Appl	331	22	30.6	11	6	US-11-004-399-2313	Sequence 2313, App
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260	23	31.9	12	6	US-11-009-731-61	Sequence 61, Appl	333	22	30.6	12	4	US-10-312-116-23	Sequence 23, Appl
261	23	31.9	12	6	US-11-051-453-68	Sequence 68, Appl	334	22	30.6	12	4	US-10-481-180-790	Sequence 790, App
262	23	31.9	13	3	US-09-876-904A-156	Sequence 156, App	335	22	30.6	12	4	US-10-738-120-16	Sequence 16, Appl
263	23	31.9	13	5	US-10-511-559-354	Sequence 254, App	336	22	30.6	12	5	US-10-783-311-112	Sequence 112, App
264	23	31.9	13	5	US-10-511-559-333	Sequence 333, App	337	22	30.6	13	3	US-09-935-682-54	Sequence 54, Appl
265	23	31.9	14	5	US-10-511-559-334	Sequence 334, App	338	22	30.6	13	4	US-10-281-478-50	Sequence 50, Appl
266	23	31.9	14	5	US-10-846-188C-5	Sequence 5, Appl1	339	22	30.6	13	4	US-10-174-613-30	Sequence 30, Appl
267	23	31.9	14	6	US-11-066-697-1409	Sequence 1409, App	340	22	30.6	13	4	US-10-116-519-30	Sequence 30, Appl
268	23	31.9	15	4	US-10-229-567-23	Sequence 23, Appl	341	22	30.6	13	4	US-10-116-519-59	Sequence 59, Appl
269	23	31.9	15	4	US-10-149-137A-9	Sequence 9, Appl1	342	22	30.6	13	4	US-10-116-519-78	Sequence 78, Appl
270	23	31.9	15	4	US-10-149-137A-101	Sequence 101, Appl	343	22	30.6	13	4	US-10-336-753-75	Sequence 75, Appl
271	23	31.9	15	5	US-10-489-802-27	Sequence 27, Appl	344	22	30.6	13	4	US-10-308-128-33	Sequence 33, Appl
272	23	31.9	15	5	US-10-769-514-84	Sequence 84, Appl	345	22	30.6	13	5	US-10-517-707A-30	Sequence 30, Appl
273	23	31.9	15	5	US-10-622-003-10	Sequence 10, Appl	346	22	30.6	13	6	US-11-033-039-1413	Sequence 1413, App
274	23	31.9	15	5	US-10-801-890-344	Sequence 344, App	347	22	30.6	14	4	US-10-174-613-41	Sequence 41, Appl
275	23	31.9	15	5	US-10-776-224-130	Sequence 130, App	348	22	30.6	14	4	US-10-308-128-42	Sequence 42, Appl
276	23	31.9	15	5	US-10-715-810-14	Sequence 14, Appl	349	22	30.6	14	5	US-10-813-338-1458	Sequence 1458, App
277	23	31.9	15	5	US-10-715-810-29	Sequence 29, Appl	350	22	30.6	14	5	US-10-946-647-1025	Sequence 1025, App
278	23	31.9	15	5	US-10-715-810-86	Sequence 86, Appl	351	22	30.6	14	5	US-10-946-647-1181	Sequence 1181, App
279	23	31.9	15	5	US-10-525-113-23	Sequence 23, Appl	352	22	30.6	15	3	US-09-908-43A-28	Sequence 42, Appl
280	23	31.9	15	5	US-10-530-061-1698	Sequence 1698, App	353	22	30.6	15	4	US-10-294-891-27	Sequence 27, Appl
281	23	31.9	15	5	US-10-530-061-1699	Sequence 1699, App	354	22	30.6	15	4	US-10-149-138-3742	Sequence 3742, App
282	23	31.9	15	5	US-10-530-061-1710	Sequence 1710, App	355	22	30.6	15	4	US-10-149-138-3846	Sequence 3846, App
283	23	31.9	15	5	US-10-530-061-1880	Sequence 1880, App	356	22	30.6	15	4	US-10-676-909-28	Sequence 28, Appl
284	23	31.9	15	6	US-11-105-725-5	Sequence 5, Appl1	357	22	30.6	15	4	US-10-149-138-3742	Sequence 3742, App
285	23	31.9	15	6	US-11-045-024-12916	Sequence 12916, A	358	22	30.6	15	4	US-10-149-138-3846	Sequence 3846, App
286	23	31.9	15	6	US-11-045-024-12972	Sequence 12972, A	359	22	30.6	15	5	US-10-801-887-42	Sequence 42, Appl
287	23	30.6	6	4	US-10-328-953-45	Sequence 45, Appl	360	22	30.6	15	5	US-10-801-838-42	Sequence 42, Appl
288	22	30.6	6	4	US-10-367-580-115	Sequence 315, App	361	22	30.6	15	5	US-10-801-509-42	Sequence 42, Appl
289	22	30.6	6	4	US-10-367-593-315	Sequence 315, App	362	22	30.6	15	5	US-10-801-486-42	Sequence 42, Appl
290	22	30.6	6	4	US-10-367-594-315	Sequence 315, App	363	22	30.6	15	5	US-10-788-992-13	Sequence 13, Appl
291	22	30.6	6	4	US-10-367-654-315	Sequence 315, App	364	22	30.6	15	5	US-10-920-313-27	Sequence 27, Appl
292	22	30.6	6	4	US-10-367-658-315	Sequence 315, App	365	22	30.6	15	5	US-10-471-894B-127	Sequence 127, App
293	22	30.6	6	4	US-10-367-674-315	Sequence 315, App	366	22	30.6	15	5	US-10-801-893-42	Sequence 42, Appl
294	22	30.6	6	4	US-10-367-674-315	Sequence 315, App	367	22	30.6	15	5	US-10-902-886-37	Sequence 37, Appl
295	22	30.6	6	5	US-10-820-067A-297	Sequence 297, App	368	22	30.6	15	6	US-11-009-460-37	Sequence 37, Appl
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297	22	30.6	8	5	US-10-958-216-1000	Sequence 1000, App	370	22	30.6	15	6	US-11-064-039-15	Sequence 15, Appl
298	22	30.6	8	6	US-11-064-416-3	Sequence 3, Appl1	371	22	30.6	15	6	US-11-065-970-57	Sequence 57, Appl
299	22	30.6	9	2	US-08-452-843A-9	Sequence 9, Appl1	372	22	30.6	15	6	US-11-045-024-12926	Sequence 12926, A
300	22	30.6	9	4	US-10-219-850-9	Sequence 9, Appl1	373	22	30.6	15	6	US-11-167-036-57	Sequence 57, Appl
301	22	30.6	9	4	US-10-353-678-15	Sequence 15, Appl	374	21	29.2	7	4	US-10-397-062-26	Sequence 26, Appl
302	22	30.6	9	4	US-10-149-138-2761	Sequence 2761, App	375	21	29.2	7	4	US-10-928-312-3	Sequence 3, Appl1
303	22	30.6	9	4	US-10-149-138-3384	Sequence 3384, App	376	21	29.2	7	5	US-10-937-042-146	Sequence 146, App
304	22	30.6	9	4	US-10-149-138-384	Sequence 384, App	377	21	29.2	7	5	US-10-885-788A-454	Sequence 454, App
305	22	30.6	9	4	US-10-364-645A-5	Sequence 5, Appl1	378	21	29.2	7	5	US-10-548-748-53	Sequence 53, Appl
306	22	30.6	9	4	US-10-364-645A-5	Sequence 36, Appl1	379	21	29.2	8	3	US-09-756-283A-88	Sequence 88, Appl
307	22	30.6	9	5	US-10-808-187-1408	Sequence 1408, App	380	21	29.2	8	4	US-10-014-440-226	Sequence 226, App
308	22	30.6	9	5	US-10-807-807-1408	Sequence 1408, App	381	21	29.2	8	4	US-10-105-735-25	Sequence 25, Appl
309	22	30.6	9	5	US-10-530-061-897	Sequence 897, App	382	21	29.2	8	4	US-10-050-271-4	Sequence 4, Appl1
310	22	30.6	9	5	US-10-530-061-992	Sequence 992, App	383	21	29.2	8	4	US-10-753-881-88	Sequence 88, Appl
311	22	30.6	9	5	US-10-530-061-1102	Sequence 1102, App	384	21	29.2	8	4	US-10-486-090-1	Sequence 1, Appl1
312	22	30.6	9	6	US-11-045-024-57	Sequence 57, Appl	385	21	29.2	8	5	US-10-903-529-79	Sequence 79, Appl
313	22	30.6	9	6	US-11-045-024-3803	Sequence 3803, App	386	21	29.2	8	5	US-10-903-529-129	Sequence 129, App
314	22	30.6	9	6	US-11-045-024-6944	Sequence 6944, App	387	21	29.2	8	5	US-10-654-601-1370	Sequence 1370, App
315	22	30.6	9	6	US-11-026-403-15	Sequence 15, Appl	388	21	29.2	8	5	US-10-937-042-79	Sequence 79, Appl
316	22	30.6	9	6	US-11-004-399-2101	Sequence 2101, App	389	21	29.2	8	5	US-10-485-788A-455	Sequence 455, App
317	22	30.6	10	3	US-09-894-018-266	Sequence 266, App	390	21	29.2	8	5	US-11-105-725-8	Sequence 8, Appl1
318	22	30.6	10	4	US-10-137-867-204	Sequence 204, App	391	21	29.2	8	6		
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394	21	29.2	8	US-11-051-411-627	Sequence 427, App	467	21	29.2	10	US-10-990-137-262	Sequence 262, App
395	21	29.2	8	US-11-045-024-129	Sequence 129, App	468	21	29.2	10	US-10-990-137-400	Sequence 400, App
396	21	29.2	8	US-11-045-024-4052	Sequence 4052, App	469	21	29.2	10	US-10-989-767A-162	Sequence 162, App
397	21	29.2	8	US-11-045-024-6334	Sequence 6334, App	470	21	29.2	10	US-10-989-767A-262	Sequence 262, App
398	21	29.2	8	US-11-045-024-6354	Sequence 6354, App	471	21	29.2	10	US-10-989-767A-420	Sequence 420, App
399	21	29.2	8	US-11-045-024-8965	Sequence 8965, App	472	21	29.2	10	US-11-105-725-9	Sequence 9, App1
400	21	29.2	8	US-11-045-024-9005	Sequence 9005, App	473	21	29.2	10	US-11-051-411-8	Sequence 8, App1
401	21	29.2	8	US-11-064-416-4	Sequence 4, App1	474	21	29.2	10	US-11-051-411-292	Sequence 292, App
402	21	29.2	9	US-09-821-819A-4	Sequence 4, App1	475	21	29.2	10	US-11-051-411-482	Sequence 482, App
403	21	29.2	9	US-09-894-018-311	Sequence 311, App	476	21	29.2	10	US-11-051-411-631	Sequence 631, App
404	21	29.2	9	US-09-779-308-413	Sequence 413, App	477	21	29.2	10	US-11-051-411-715	Sequence 715, App
405	21	29.2	9	US-09-898-860-124	Sequence 124, App	478	21	29.2	10	US-11-051-411-924	Sequence 924, App
406	21	29.2	9	US-10-215-272-43	Sequence 43, App1	479	21	29.2	10	US-11-000-328-27	Sequence 27, App1
407	21	29.2	9	US-10-716-326-43	Sequence 43, App1	480	21	29.2	10	US-11-045-024-5229	Sequence 5229, App
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433	21	29.2	10	US-09-935-430-262	Sequence 262, App	506	21	29.2	11	US-10-801-938-122	Sequence 122, App
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435	21	29.2	10	US-09-572-404B-3147	Sequence 3147, App	508	21	29.2	11	US-10-801-938-122	Sequence 122, App
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437	21	29.2	10	US-09-896-923-8	Sequence 8, App1	510	21	29.2	11	US-10-801-938-122	Sequence 122, App
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440	21	29.2	10	US-10-277-292-162	Sequence 162, App	513	21	29.2	11	US-11-022-327-5	Sequence 5, App1
441	21	29.2	10	US-10-277-292-262	Sequence 262, App	514	21	29.2	11	US-11-022-327-5	Sequence 5, App1
442	21	29.2	10	US-10-277-292-420	Sequence 420, App	515	21	29.2	11	US-11-022-327-5	Sequence 5, App1
443	21	29.2	10	US-10-280-340-162	Sequence 162, App	516	21	29.2	11	US-11-022-327-5	Sequence 5, App1
444	21	29.2	10	US-10-280-340-262	Sequence 262, App	517	21	29.2	11	US-11-022-327-5	Sequence 5, App1
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447	21	29.2	10	US-10-223-650-8	Sequence 8, App1	520	21	29.2	11	US-11-022-327-5	Sequence 5, App1
448	21	29.2	10	US-10-376-647B-33	Sequence 33, App1	521	21	29.2	11	US-11-022-327-5	Sequence 5, App1
449	21	29.2	10	US-10-351-608A-33	Sequence 33, App1	522	21	29.2	11	US-11-022-327-5	Sequence 5, App1
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451	21	29.2	10	US-10-432-234A-448	Sequence 448, App	524	21	29.2	11	US-11-022-327-5	Sequence 5, App1
452	21	29.2	10	US-10-432-234A-449	Sequence 449, App	525	21	29.2	11	US-11-022-327-5	Sequence 5, App1
453	21	29.2	10	US-10-432-234A-450	Sequence 450, App	526	21	29.2	11	US-11-022-327-5	Sequence 5, App1
454	21	29.2	10	US-10-432-234A-451	Sequence 451, App	527	21	29.2	11	US-11-022-327-5	Sequence 5, App1
455	21	29.2	10	US-10-432-234A-452	Sequence 452, App	528	21	29.2	11	US-11-022-327-5	Sequence 5, App1
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457	21	29.2	10	US-10-432-234A-454	Sequence 454, App	530	21	29.2	11	US-11-022-327-5	Sequence 5, App1
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461	21	29.2	10	US-10-654-601-498	Sequence 498, App	534	21	29.2	11	US-11-022-327-5	Sequence 5, App1
462	21	29.2	10	US-10-654-601-1021	Sequence 1021, App	535	21	29.2	11	US-11-022-327-5	Sequence 5, App1
463	21	29.2	10	US-10-654-601-1163	Sequence 1163, App	536	21	29.2	11	US-11-022-327-5	Sequence 5, App1
464	21	29.2	10	US-10-936-237-14	Sequence 14, App1	537	21	29.2	11	US-11-022-327-5	Sequence 5, App1
465	21	29.2	10	US-10-839-456-8	Sequence 8, App1	538	21	29.2	11	US-11-022-327-5	Sequence 5, App1
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685 21 29.2 15 6 US-11-009-460-13 Sequence 13, Appl
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688 21 29.2 15 6 US-11-136-186-43 Sequence 43, Appl
689 21 29.2 15 6 US-11-069-543-163 Sequence 163, App
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691 21 29.2 15 6 US-11-032-794-5 Sequence 5, Appl1
692 21 29.2 15 6 US-11-000-365-5 Sequence 13078, A
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703 21 29.2 15 6 US-10-310-674A-22 Sequence 19, Appl
704 21 29.2 15 6 US-10-374-466-19 Sequence 26, Appl
705 21 29.2 15 6 US-11-063-771-26 Sequence 26, Appl
706 21 29.2 15 6 US-11-104-353-26 Sequence 26, Appl
707 21 29.2 15 6 US-10-862-195-165 Sequence 23, Appl
708 21 29.2 15 6 US-10-862-195-165 Sequence 166, App
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740 21 29.2 15 6 US-10-820-067A-110 Sequence 110, App
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753 21 29.2 15 6 US-10-094-699-67 Sequence 67, Appl
754 21 29.2 15 6 US-10-172-597-167 Sequence 187, App
755 21 29.2 15 6 US-10-277-292-560 Sequence 560, App
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757 21 29.2 15 6 US-10-334-726-109 Sequence 109, App
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758 20 27.8 9 4 US-10-117-937-412 Sequence 412, App
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765 20 27.8 9 5 US-10-715-976-39 Sequence 39, Appl1
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767 20 27.8 9 5 US-10-990-137-560 Sequence 560, App
768 20 27.8 9 5 US-10-491-096-119 Sequence 129, App
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770 20 27.8 9 5 US-10-530-061-206 Sequence 206, App
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772 20 27.8 9 6 US-11-012-787-187 Sequence 187, App
773 20 27.8 9 6 US-11-105-725-6 Sequence 6, Appl1
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776 20 27.8 9 6 US-11-045-024-132 Sequence 132, Appl
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778 20 27.8 9 6 US-11-045-024-8214 Sequence 8214, Ap
779 20 27.8 9 6 US-11-045-024-8933 Sequence 8933, Ap
780 20 27.8 10 2 US-08-996-140-13 Sequence 1117, A
781 20 27.8 10 3 US-09-056-160B-95 Sequence 13, Appl
782 20 27.8 10 3 US-09-056-160B-95 Sequence 95, Appl
783 20 27.8 10 3 US-09-834-765-97 Sequence 97, Appl
784 20 27.8 10 3 US-09-834-765-433 Sequence 93, App
785 20 27.8 10 3 US-09-834-765-433 Sequence 473, App
786 20 27.8 10 3 US-09-891-823-73 Sequence 73, Appl
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788 20 27.8 10 3 US-09-935-430-518 Sequence 417, App
789 20 27.8 10 3 US-09-572-404B-1350 Sequence 518, App
790 20 27.8 10 3 US-09-572-404B-1352 Sequence 1350, Ap
791 20 27.8 10 3 US-09-572-404B-1934 Sequence 1934, Ap
792 20 27.8 10 3 US-09-572-404B-3710 Sequence 2710, Ap
793 20 27.8 10 3 US-09-572-404B-3116 Sequence 3116, Ap
794 20 27.8 10 3 US-09-820-053A-142 Sequence 142, Ap
795 20 27.8 10 3 US-09-573-822C-36 Sequence 36, Appl
796 20 27.8 10 3 US-09-573-822C-372 Sequence 372, Appl
797 20 27.8 10 3 US-09-573-822C-621 Sequence 621, App
798 20 27.8 10 3 US-09-573-822C-672 Sequence 672, App
799 20 27.8 10 3 US-09-899-575-130 Sequence 130, App
800 20 27.8 10 3 US-09-833-245-529 Sequence 529, App
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ALIGNMENTS

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RESULT 1
US-10-884-862-219
; Sequence 219, Application US/10884862
; Publication No. US20050048071A1
GENERAL INFORMATION:
APPLICANT: BAE, Joo-eun
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
FILE REFERENCE: 047940-0239
CURRENT APPLICATION NUMBER: US/10/884, 862
PRIOR FILING DATE: 2004-07-02
PRIOR APPLICATION NUMBER: US 60/484689
NUMBER OF SEQ ID NOS: 328
SOFTWARE: PatentIn version 3.2
SEQ ID NO 219
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Homo sapiens
US-10-884-862-219
Query Match 40.3%; Score 29; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. 1.9e+06;
Matches 5; Conservative 3; Mismatches 0; Gaps 0;
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QY 8 SVKSLVIG 15

Db 1 SIOSLFLG 8

RESULT 2

US-10-820-067A-361
 ; Sequence 361, Application US/10820067A
 ; Publication No. US20050214312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fletcher, J.
 ; APPLICANT: Prince-Cohane, K.
 ; APPLICANT: Mehta, S.
 ; APPLICANT: Siusarewicz, P.
 ; APPLICANT: Andjelic, S.
 ; APPLICANT: Barber, B.
 ; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
 ; TITLE OF INVENTION: VACCINES AND IMMUNOTHERAPIES
 ; FILE REFERENCE: 8449-406-999
 ; CURRENT APPLICATION NUMBER: US/10/820,067A
 ; CURRENT FILING DATE: 2004-04-08
 ; PRIOR APPLICATION NUMBER: 60/462,469
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: 60/463,746
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: 60/503,417
 ; PRIOR FILING DATE: 2003-09-16
 ; NUMBER OF SEQ ID NOS: 926
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 361
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Heat shock protein binding motif
 US-10-820-067A-361

Query Match 38.9%; Score 28; DB 5; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.9e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15
 DB 1 VKKLYIG 7

RESULT 3

US-10-776-521B-152
 ; Sequence 152, Application US/10776521B
 ; Publication No. US20050202033A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fletcher, Jessica
 ; APPLICANT: Prince-Cohane, Kenya
 ; APPLICANT: Mehta, Sunil
 ; APPLICANT: Siusarewicz, Paul
 ; APPLICANT: Andjelic, Sofija
 ; APPLICANT: Barber, Brian
 ; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
 ; TITLE OF INVENTION: IMMUNOTHERAPIES
 ; FILE REFERENCE: 8449-405-999
 ; CURRENT APPLICATION NUMBER: US/10/776,521B
 ; CURRENT FILING DATE: 2004-02-12
 ; PRIOR APPLICATION NUMBER: 60/503,417
 ; PRIOR FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/463,746
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: 60/462,469
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: 60/447,142
 ; PRIOR FILING DATE: 2003-02-13
 ; NUMBER OF SEQ ID NOS: 419
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 8

TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Heat shock protein binding domain with a terminal
 ; OTHER INFORMATION: Trp residue
 US-10-776-521B-152

Query Match 38.9%; Score 28; DB 5; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.9e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15
 DB 1 VKKLYIG 7

RESULT 4

US-10-820-067A-648
 ; Sequence 648, Application US/10820067A
 ; Publication No. US20050214312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fletcher, J.
 ; APPLICANT: Prince-Cohane, K.
 ; APPLICANT: Mehta, S.
 ; APPLICANT: Siusarewicz, P.
 ; APPLICANT: Andjelic, S.
 ; APPLICANT: Barber, B.
 ; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
 ; TITLE OF INVENTION: VACCINES AND IMMUNOTHERAPIES
 ; FILE REFERENCE: 8449-406-999
 ; CURRENT APPLICATION NUMBER: US/10/820,067A
 ; CURRENT FILING DATE: 2004-04-08
 ; PRIOR APPLICATION NUMBER: 60/462,469
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: 60/463,746
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: 60/503,417
 ; PRIOR FILING DATE: 2003-09-16
 ; NUMBER OF SEQ ID NOS: 926
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 648
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Heat shock protein binding domain with a terminal
 ; OTHER INFORMATION: Trp residue
 US-10-820-067A-648

Query Match 38.9%; Score 28; DB 5; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.9e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15
 DB 1 VKKLYIG 7

RESULT 5

US-10-943-793-17
 ; Sequence 17, Application US/10943793
 ; Publication No. US20060063214A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALPER, OZGE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
 ; TITLE OF INVENTION: NEOPLASTIC DISEASE
 ; FILE REFERENCE: BIOS-003
 ; CURRENT APPLICATION NUMBER: US/10/943,793
 ; CURRENT FILING DATE: 2004-09-17
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 15


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; TYPE: PRT
; ORGANISM: H. sapien
US-10-943-793-17

Query Match      37.5%; Score 27; DB 5; Length 15;
Best Local Similarity 85.7%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PFSVAKS 8
       |||||
Db      2 PFSVAVS 8

RESULT 6
US-09-852-910-81
; Sequence 81, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-852-910-81

Query Match      36.1%; Score 26; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 VAKSVKSLYL 14
       ||::||:|
Db      1 IAKNLKSMGL 10

RESULT 7
US-10-411-336A-81
; Sequence 81, Application US/10411336A
; Publication No. US20040018558A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, ANNETTE
; APPLICANT: HAMM, HEIDI
; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 2661-102
; CURRENT APPLICATION NUMBER: US/10/411,336A
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/852910
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/275472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-411-336A-81

Query Match      36.1%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 VAKSVKSLYL 14
       ||::||:|
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Db      1 IAKNLKSMGL 10

RESULT 8
US-09-563-222-35
; Sequence 35, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 31098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-35

Query Match      36.1%; Score 26; DB 3; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 SVAKSVKSLYL 14
       |:|||||
Db      1 SASSSVSSSYL 11

RESULT 9
US-10-461-878-1
; Sequence 1, Application US/10461878
; Publication No. US20040057902A1
; GENERAL INFORMATION:
; APPLICANT: GOLD, DAVID V.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY cPAM4
; FILE REFERENCE: 018733/1246
; CURRENT APPLICATION NUMBER: US/10/461,878
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,313
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: chimerized PAM4 antibody fragment
US-10-461-878-1

Query Match      36.1%; Score 26; DB 4; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 SVAKSVKSLYL 14
       |:|||||
Db      1 SASSSVSSSYL 11

RESULT 10
US-10-783-950-35
; Sequence 35, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
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APPLICANT: HEIN, MICH B.
FILE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/10/783,950
PRIOR FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: US/09/563,222
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 12
TYPE: .PRT
ORGANISM: Mus musculus
US-10-783-950-35
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Query Match          36.1%; Score 26; DB 4; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY 4 SVAKSVKSLYL 14
    | : ||| |
    1 SASSSVSSSYL 11
```

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RESULT 11
US-10-461-885-1
Sequence 1, Application US/10461885
Publication No. US20050014207A1
GENERAL INFORMATION:
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: HANSEN, HANS J.
APPLICANT: QU, ZHENGXING
TITLE OF INVENTION: MONOCLONAL ANTIBODY hPAM4
FILE REFERENCE: 018733-1215
CURRENT APPLICATION NUMBER: US/10/461,885
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/388,314
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 12
TYPE: .PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized PAM4
US-10-461-885-1
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Query Match          36.1%; Score 26; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY 4 SVAKSVKSLYL 14
    | : ||| |
    1 SASSSVSSSYL 11
```

```
RESULT 12
US-10-507-662-11
Sequence 11, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136CT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
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PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 12
TYPE: .PRT
ORGANISM: Homo sapiens
US-10-507-662-11
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```
Query Match          36.1%; Score 26; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 SVAKSVKSLYL 14
    | : ||| |
    1 SASSSVSSSYL 11
```

```
RESULT 13
US-09-820-649-319
Sequence 319, Application US/09820649
Publication No. US2003019683A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 83 Human Secreted Proteins
FILE REFERENCE: P2012P1
CURRENT APPLICATION NUMBER: US/09/820,649
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US/09/236,557
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,218
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,236
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,215
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,211
PRIOR FILING DATE: 1997-07-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 319
LENGTH: 14
TYPE: .PRT
ORGANISM: Homo sapiens
US-09-820-649-319
```

```
Query Match          36.1%; Score 26; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 PPSVAKSV 9
    ||| : |
    3 PPSISYSI 10
```

```
RESULT 14
US-10-160-162-319
Sequence 319, Application US/10160162
Publication No. US2003016541A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 83 Human Secreted Proteins
/ FILE REFERENCE: P2012P2
/ CURRENT APPLICATION NUMBER: US/10/160,162
/ CURRENT FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/295,558
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/236,557
/ PRIOR FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: PCT/US98/15949
/ PRIOR FILING DATE: 1998-07-29
/ PRIOR APPLICATION NUMBER: 60/054,212
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,209
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,234
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,218
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,214
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,236
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,215
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,211
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,217
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,213
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/055,968
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,969
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,972
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/056,561
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,534
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,729
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,543
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,727
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,554
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,730
/ PRIOR FILING DATE: 1997-08-19
/ NUMBER OF SEQ ID NOS: 353
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 319
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-160-162-319

Query Match      36.1%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 PPSVAKSV 9
      |||::|:
Db      3 PPSISYSI 10

RESULT 15
US-10-936-773-319
; Sequence 319, Application US/10936773
; Publication No. US20050037467A1

/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 83 Human Secreted Proteins
/ FILE REFERENCE: P2012P2
/ CURRENT APPLICATION NUMBER: US/10/936,773
/ CURRENT FILING DATE: 2004-09-09
/ PRIOR APPLICATION NUMBER: US/10/160,162
/ PRIOR FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/295,558
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/236,557
/ PRIOR FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: PCT/US98/15949
/ PRIOR FILING DATE: 1998-07-29
/ PRIOR APPLICATION NUMBER: 60/054,212
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,209
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,234
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,218
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,214
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,216
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,236
/ PRIOR FILING DATE: 1997-07-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 353
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 319
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-936-773-319

Query Match      36.1%; Score 26; DB 5; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 PPSVAKSV 9
      |||::|:
Db      3 PPSISYSI 10

RESULT 16
US-09-907-969-500
; Sequence 500, Application US/09907969
; Publication No. US20030091580A1
/ GENERAL INFORMATION:
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: King, Gordon E.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Fling, Steven P.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary Richard
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedwick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Hill, Paul
/ APPLICANT: Albone, Bart
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: AND DIAGNOSIS OF OVARIAN CANCER
/ CURRENT APPLICATION NUMBER: US/09/907,969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 500
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-500
```

Query Match 36.1%; Score 26; DB 3; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
|:|:|
Db 2 PYSIDKD--SLYL 12

RESULT 17

US-10-198-053-500
; Sequence 500, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-500

Query Match 36.1%; Score 26; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
|:|:|
Db 2 PYSIDKD--SLYL 12

RESULT 18
US-10-431-096-289
; Sequence 289, Application US/10431096
; Publication No. US20040086896A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0108A CIP
; CURRENT APPLICATION NUMBER: US/10/431.096
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/284,962
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 10/126,103
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/286,645
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/346,986
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 289
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-431-096-289

Query Match 36.1%; Score 26; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVK 10
|:|:|:|

Db 2 VPISDSKSIQ 11

RESULT 19
US-10-860-790-500
; Sequence 500, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860.790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-500

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
|:|:|
Db 2 PYSIDKD--SLYL 12

RESULT 20
US-10-676-909-53
; Sequence 53, Application US/10676909
; Publication No. US20040086521A1
; GENERAL INFORMATION:
; APPLICANT: KROPSHOFER, H.
; APPLICANT: VOGT, A.
; TITLE OF INVENTION: Method for the identification of antigenic peptides associated t
; FILE REFERENCE: 21388
; CURRENT APPLICATION NUMBER: US/10/676.909
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: EP 02022223.8
; PRIOR FILING DATE: 2002-02-10
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-676-909-53

Query Match 35.4%; Score 25.5; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 4 SVAKSVKSL-YL 14
|:|:|:|
Db 2 AVTKSIRSIPLYL 13

RESULT 21
US-10-676-909-54
; Sequence 54, Application US/10676909
; Publication No. US20040086521A1
; GENERAL INFORMATION:
; APPLICANT: KROPSHOFER, H.
; APPLICANT: VOGT, A.
; TITLE OF INVENTION: Method for the identification of antigenic peptides associated t

```
/ TITLE OF INVENTION: diseases
/ FILE REFERENCE: 21388
/ CURRENT APPLICATION NUMBER: US/10/676,909
/ CURRENT FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: EP 02022223.8
/ PRIOR FILING DATE: 2002-02-10
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 54
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-676-909-54

Query Match          35.4%; Score 25; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      4 SVAKSVKSL-YL 14
       : |||:|:|
Db      3 AVVKSRISPYL 14

RESULT 22
US-09-920-480B-9
/ Sequence 9, Application US/09920480B
/ Publication No. US20040014697A1
/ GENERAL INFORMATION:
/ APPLICANT: Nicolette, Charles A.
/ TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
/ FILE REFERENCE: G2 2063.10
/ CURRENT APPLICATION NUMBER: US/09/920,480B
/ CURRENT FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 09/249,272
/ PRIOR FILING DATE: 1999-02-11
/ PRIOR APPLICATION NUMBER: 60/103,229
/ PRIOR FILING DATE: 1998-10-05
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FastSeq For Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-920-480B-9

Query Match          34.7%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSV 5
       : |||
Db      4 VPFSV 8

RESULT 23
US-10-333-430-17
/ Sequence 17, Application US/10333430
/ Publication No. US20040072240A1
/ GENERAL INFORMATION:
/ APPLICANT: INSEERM
/ APPLICANT: INSTITUT GUSTAVE ROUSSY
/ APPLICANT: KOSMATOPOULOS, Kostas
/ APPLICANT: TOURDOT, Sophie
/ APPLICANT: SCARDINO, Antonio
/ TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
/ TITLE OF INVENTION: IMMUNOTHERAPY
/ FILE REFERENCE: 33339/259034
/ CURRENT APPLICATION NUMBER: US/10/333,430
/ CURRENT FILING DATE: 2003-10-02
/ PRIOR APPLICATION NUMBER: FR 0009591
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 70
```

```
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-10-333-430-17

Query Match          34.7%; Score 25; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSV 5
       : |||
Db      4 VPFSV 8

RESULT 24
US-09-847-185-30
/ Sequence 30, Application US/09847185
/ Patent No. US20020076392A1
/ GENERAL INFORMATION:
/ APPLICANT: SOO HOO, William
/ TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
/ COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
/ RESPONSE USING SAME
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: CAMPBELL & FLORES, LLP
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/847,185
/ FILING DATE: 01-May-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/201,931
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-1M 2442
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619)535-9001
/ TELEFAX: (619)535-8949
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-847-185-30

Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSV 5
       : |||
Db      5 VPFSV 9

RESULT 25
```

```
US-09-862-260A-3
; Sequence 3, Application US/09862260A
; Patent No. US20020082217A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: 126881210200
; CURRENT APPLICATION NUMBER: US/09/862,260A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/208,955
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/267,877
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-260A-3
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VPFVS 5
        |||||
Db      5 VPFVS 9
```

```
RESULT 26
US-09-862-260A-23
; Sequence 23, Application US/09862260A
; Patent No. US20020082217A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: 126881210200
; CURRENT APPLICATION NUMBER: US/09/862,260A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/208,955
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/267,877
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-260A-23
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VPFVS 5
        |||||
Db      5 VPFVS 9
```

```
RESULT 27
US-09-923-831-31
; Sequence 31, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07
```

```
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-31
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VPFVS 5
        |||||
Db      5 VPFVS 9
```

```
RESULT 28
US-09-872-832-45
; Sequence 45, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(9)
; OTHER INFORMATION: gp-100 modified peptide
US-09-872-832-45
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VPFVS 5
        |||||
Db      5 VPFVS 9
```

```
RESULT 29
US-09-766-889A-43
; Sequence 43, Application US/09766889A
; Patent No. US2002016454A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
```

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-43
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 30
US-09-812-238B-3
; Sequence 3, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-3
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 31
US-09-812-238B-5
; Sequence 5, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-5
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 32
US-09-812-238B-7
; Sequence 7, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-7
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 33
US-09-812-238B-9
; Sequence 9, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-9
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 34
US-09-812-238B-11
; Sequence 11, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-11
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
```

Db 5 VPFSV 9

RESULT 35
US-09-812-238B-13
; Sequence 13, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-13

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 36
US-09-812-238B-15
; Sequence 15, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-15

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 37
US-09-812-238B-17
; Sequence 17, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-812-238B-17

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 38
US-09-812-238B-19
; Sequence 19, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-19

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 39
US-09-909-460-62
; Sequence 62, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-62

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 40
US-09-865-548A-42
; Sequence 42, Application US/09865548A

Publication No. US20030096298A1
GENERAL INFORMATION:
APPLICANT: Barnea, Eilon
APPLICANT: Beer, Ilan
APPLICANT: Ziv, Tamir
APPLICANT: Admon, Arie
TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
FILE REFERENCE: 01/22080
CURRENT APPLICATION NUMBER: US/09/865,548A
PRIORITY FILING DATE: 2001-05-16
PRIORITY FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 42
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-865-548A-42

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VFPSV 5
Db 5 VFPSV 9

RESULT 41
US-09-898-860-48
Sequence 48, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-898-860-48

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VFPSV 5
Db 5 VFPSV 9

RESULT 42
US-09-898-860-83
Sequence 83, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-898-860-83

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 43

US-09-898-860-84
; Sequence 84, Application US/09898860
; Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEX: 421792

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 84:

US-09-898-860-84

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 44

US-09-898-860-85

; Sequence 85, Application US/09898860

; Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEX: 421792

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 85:

US-09-898-860-85

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 45

US-09-898-860-86

; Sequence 86, Application US/09898860

; Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-898-860-86

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
|||
5 VPPSV 9

Db 5 VPPSV 9

RESULT 46
US-09-898-860-87
Sequence 87, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-09-898-860-87

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
|||
5 VPPSV 9

Db 5 VPPSV 9

RESULT 47
US-09-898-860-88
Sequence 88, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown

TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-898-860-88

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 48
US-09-898-860-89
Sequence 89, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-898-860-89

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 49
US-09-898-860-90
Sequence 90, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-898-860-90

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 50
US-09-898-860-91

Sequence 91, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-898-860-91
Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPPSV 5
Db 5 VPPSV 9
RESULT 51
US-09-898-860-92
Sequence 92, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-898-860-92
Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPPSV 5
Db 5 VPPSV 9
RESULT 52
US-09-898-860-93
Sequence 93, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-898-860-93

Query Match 34.7%; Score 25; DB 3; Length 9;
Best local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 53
US-09-898-860-94
Sequence 94, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-898-860-94

Query Match 34.7%; Score 25; DB 3; Length 9;
Best local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 54
US-09-898-860-95
Sequence 95, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-898-860-95

Query Match 34.7%; Score 25; DB 3; Length 9;
Best local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 55
US-09-898-860-96
Sequence 96, Application US/09898860
Publication No. US20030144482A1

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-898-860-96
Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
|||
5 VPFSV 9
Db
RESULT 56
US-09-898-860-97
Sequence 97, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-898-860-97
Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
|||
5 VPFSV 9
Db
RESULT 57
US-09-898-860-98
Sequence 98, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-898-860-98

Query Match 34.7% Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 58

US-09-898-860-99
Sequence 99, Application US/09898860
Publication No. US20030144482A1

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-09-898-860-99

Query Match 34.7% Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 59

US-09-898-860-100
Sequence 100, Application US/09898860
Publication No. US20030144482A1

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-09-898-860-100

Query Match 34.7% Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5

Db 5 VPFSV 9

|||||

RESULT 60

US-09-898-860-101

Sequence 101, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-09-898-860-101

Query Match 34.7%; Score 25; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5

|||||

Db 5 VPFSV 9

RESULT 61

US-09-898-860-102

Sequence 102, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

|||||

METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 102:

US-09-898-860-102

Query Match 34.7%; Score 25; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5

|||||

Db 5 VPFSV 9

RESULT 62

US-09-898-860-103

Sequence 103, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS


```
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/998,860
  FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/267,439
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US/08/417,174
  FILING DATE: 05-APR-1995
  APPLICATION NUMBER: US/08/231,565
  FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
  NAME: CAROL M. GRUPPI
  REGISTRATION NUMBER: 37,341
  REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 758-4800
  TELEFAX: (212) 751-6849
  TELEX: 421792
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
  LENGTH: 9
  TYPE: amino acid
  STRANDEDNESS: Unknown
  TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-898-860-103
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Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPPSV 5
        |||||
Db      5 VPPSV 9
```

```
RESULT 63
US-09-920-480B-5
; Sequence 5, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-480B-5
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPPSV 5
        |||||
Db      5 VPPSV 9
```

```
RESULT 64
US-09-920-480B-6
; Sequence 6, Application US/09920480B
; Publication No. US20040014697A1
```

```
GENERAL INFORMATION:
  APPLICANT: Nicolette, Charles A.
  TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
  FILE REFERENCE: GZ 2063.10
CURRENT APPLICATION NUMBER: US/09/920,480B
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/249,272
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/103,229
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-920-480B-6
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPPSV 5
        |||||
Db      5 VPPSV 9
```

```
RESULT 65
US-09-920-480B-7
; Sequence 7, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-480B-7
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```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPPSV 5
        |||||
Db      5 VPPSV 9
```

```
RESULT 66
US-09-920-480B-8
; Sequence 8, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-920-480B-8
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 67
US-09-872-836-62
/ Sequence 62, Application US/09872836
/ Publication No. US20040142475A1
/ GENERAL INFORMATION:
/ APPLICANT: Barman, Shikha P.
/ APPLICANT: McKeever, Una
/ APPLICANT: Hedley, Mary Lynne
/ TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
/ FILE REFERENCE: 08191-018001
/ CURRENT APPLICATION NUMBER: US/09/872,836
/ CURRENT FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: US 60/208,830
/ PRIOR FILING DATE: 2000-06-02
/ NUMBER OF SEQ ID NOS: 120
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 62
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-872-836-62
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 68
US-10-106-487-3
/ Sequence 3, Application US/10106487
/ Publication No. US20020164721A1
/ GENERAL INFORMATION:
/ APPLICANT: FIRAT, HUSEYIN
/ APPLICANT: LEMONNIER, FRANCOIS
/ APPLICANT: LANGLADE-DEMOYEN, PIERRE
/ APPLICANT: MITCHEL, MARIE-LOUISE
/ TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION
/ TITLE OF INVENTION: OF
/ TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
/ FILE REFERENCE: 03495.0196 SEQUENCE LISTING
/ CURRENT APPLICATION NUMBER: US/10/106,487
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: 09/675,673
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/158,356
/ PRIOR FILING DATE: 1999-10-12
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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US-10-106-487-3

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 69
US-10-047-539-6
/ Sequence 6, Application US/10047539
/ Publication No. US2002017547A1
/ GENERAL INFORMATION:
/ APPLICANT: KOLLING, KARIN
/ APPLICANT: PAVLOVIC, JOVAN
/ APPLICANT: NAMRATH, MICHAEL
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING
/ TITLE OF INVENTION: CANCER
/ FILE REFERENCE: VOS-27
/ CURRENT APPLICATION NUMBER: US/10/047,539
/ CURRENT FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: EP 01 10 0914.9
/ PRIOR FILING DATE: 2001-01-16
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-047-539-6
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 70
US-10-073-300-1
/ Sequence 1, Application US/10073300
/ Publication No. US20030003535A1
/ GENERAL INFORMATION:
/ APPLICANT: Reiter, Yoram
/ TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
/ FILE REFERENCE: 02/23339
/ CURRENT APPLICATION NUMBER: US/10/073,300
/ CURRENT FILING DATE: 2002-06-25
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-073-300-1
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

RESULT 71

US-10-108-511-8
; Sequence 8, Application US/10108511
; Publication No. US20030017134A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Avital, Lev
; TITLE OF INVENTION: METHODS AND PHARMACEUTICAL COMPOSITIONS FOR IMMUNE DECEPTION,
; FILE REFERENCE: PARTICULARLY USEFUL IN THE TREATMENT OF CANCER
; FILE REFERENCE: 01/23109
; CURRENT APPLICATION NUMBER: US/10/108,511
; CURRENT FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: HLA-A2-restricted synthetic peptide, derived from the melanoma d
; OTHER INFORMATION: fferentiation antigen gp100
US-10-108-511-8

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 72
US-10-080-013-4
; Sequence 4, Application US/10080013
; Publication No. US20030077248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Lecurcy, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Maria
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-4

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 73
US-10-161-097-28
; Sequence 28, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADSEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION

; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10/161,097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-10-161-097-28

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 74
US-10-224-286-30
; Sequence 30, Application US/10224286
; Publication No. US20030108517A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/224,286
; FILING DATE: 19-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-224-286-30

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 75
US-10-170-832-72
; Sequence 72, Application US/10170832
; Publication No. US20030170792A1
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valérie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortals, Jürgen
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-72

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 76
US-10-371-942-1
; Sequence 1, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoozenboom, Henricus Renertus Jacobus Matthaeus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-1

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 77
US-10-245-871-425
; Sequence 425, Application US/10245871
; Publication No. US2003023594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 425
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-425

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 78
US-10-465-811-73
; Sequence 73, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-811-73

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 79
US-10-168-417A-5
; Sequence 5, Application US/10168417A
; Publication No. US20040009185A1
; GENERAL INFORMATION:

```
/ APPLICANT: Emtage, Peter
/ APPLICANT: Barber, Brian
/ APPLICANT: Sambhara, Suryprakash
/ APPLICANT: Sia, Charles Dwo Yuan
/ TITLE OF INVENTION: Enhancing the Immune Response to an Antigen by Presensitizing with
/ FILE REFERENCE: 11014-18-US
/ CURRENT APPLICATION NUMBER: US/10/168,417A
/ CURRENT FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: US 60/174,587
/ PRIOR FILING DATE: 2000-01-05
/ PRIOR APPLICATION NUMBER: PCT/CA01/00005
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide, amino acids 209-217 of gp 100, referred to as
US-10-168-417A-5
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```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VPFSV 5
         |||||
Db      5 VPFSV 9
```

```
RESULT 80
US-10-168-417A-7
/ Sequence 7, Application US/10168417A
/ Publication No. US20040009185A1
/ GENERAL INFORMATION:
/ APPLICANT: Emtage, Peter
/ APPLICANT: Barber, Brian
/ APPLICANT: Sambhara, Suryprakash
/ APPLICANT: Sia, Charles Dwo Yuan
/ TITLE OF INVENTION: Enhancing the Immune Response to an Antigen by Presensitizing with
/ FILE REFERENCE: 11014-18-US
/ CURRENT APPLICATION NUMBER: US/10/168,417A
/ CURRENT FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: US 60/174,587
/ PRIOR FILING DATE: 2000-01-05
/ PRIOR APPLICATION NUMBER: PCT/CA01/00005
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide, amino acids 209-217 of modified gp 100, referred
US-10-168-417A-7
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      1 VPFSV 5
         |||||
Db      5 VPFSV 9
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Search completed: July 12, 2006, 05:54:11
Job time : 184 secs

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